

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

722 752  
 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
 thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser  
  
 782 812  
 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
 trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys  
  
 842 | Cadherin Cleavage | 872  
 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
 val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val  
  
 902 932  
 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
 val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys  
  
 962 992  
 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
 asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly  
  
 1022 1052  
 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
 phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr  
  
 1082 1112  
 TCTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
 leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro  
  
 1142 1172  
 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
 leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu  
  
 1202 1232 | Cadherin EC  
 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
 asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg  
  
 xxx 1292  
 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
 glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu  
  
 1322 1352  
 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
 lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala  
  
 1382 1412/471  
 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
 arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile  
  
 1442 1472  
 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
 asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 1 (cont.)

1502	1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC	
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn	
1562	1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA	
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser	
1622	1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT	
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp	
1682	1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA	
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln	
1742	1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT	
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile	
1802	1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT	
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe	
1862	1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC	
thr tyr trp asn lys ala ser thr ser glu leu met asp phe thr ile ser glu val	
1922	1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG	
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu	
1982	2012
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA	
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly	
2042	2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC	
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his	
2102	2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT	
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala	
2162	2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC	
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn	
2222	2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG	
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu	
2282	2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG	

FIG. 1 (cont.)

cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552  
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 |xxxxxxxxxxxxxxxxxxxx Predicted  
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxx|  
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

3002 3032  
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092  
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT

FIG.1 (cont.)

cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

3122

3155

ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT  
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182

3212

ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242

3272

TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC  
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302

3332

CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362

3392

GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC  
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422

3452

TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482

3512

TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC  
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys arg ile

3542

3572

CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG  
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602

xxx Coiled-Coil 1 xxxxxxxxxxxxxxxx 3632 xxxx Coiled-Coil 1 xxxxxxxxxxxxxxxx  
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA  
ser lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662

3692

xxxxxxxxxxxxxxxxxxxxx| CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT  
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722

3752

GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG  
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782

3812

xxxxxxxxxxxxxxxxxxxxx| CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA  
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842

3872

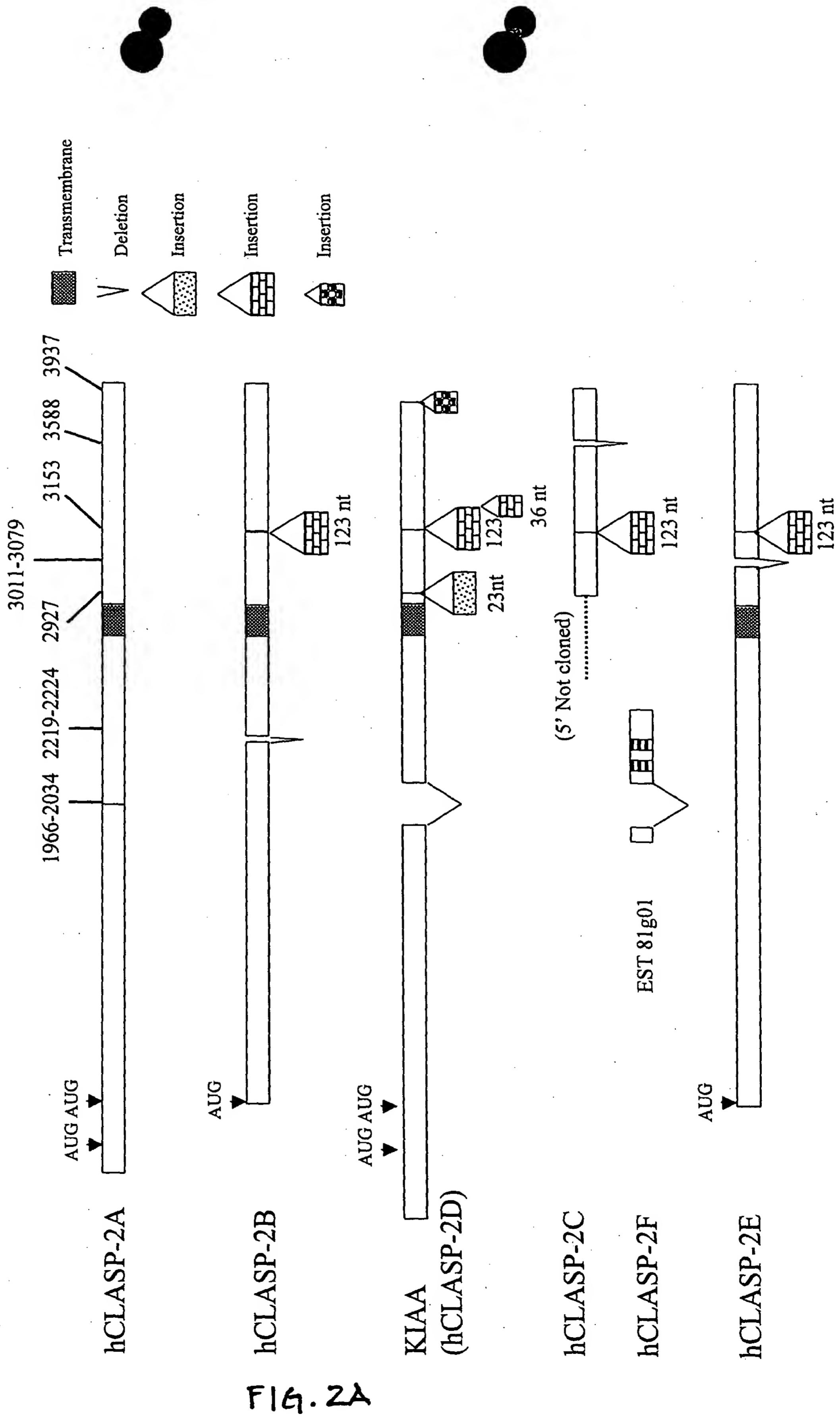
xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA

FIG. 1 (cont.)

arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu  
3902 xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3932 xxxxx|  
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr  
3962 3992  
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr  
4022 |xxxxx PBM xxxx|  
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser val val STP  
4082 4112  
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG  
4142 4172  
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT  
4202 4232  
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG  
4262 4292  
GCA ATA TTC AAA GTT TTG ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA  
4322 4352  
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG  
4382 4412  
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG  
4442 4472  
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA  
4502 4532  
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA  
4562 4592  
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT  
4622 4652  
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC  
4682 4712  
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA  
4742 4772  
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC  
4802  
TTT ACT

FIG. 1 (cont.)

(Nucleotide position for insertions and deletion are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)



2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

722 752  
 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
 thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812  
 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
 trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 872  
 Cadherin Cleavage  
 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
 val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932  
 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
 val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992  
 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC ATG GAC AGG GGC  
 asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052  
 GTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
 phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112  
 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
 leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172  
 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
 leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 Cadherin EC  
 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
 asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx 1292  
 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
 glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352  
 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
 lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412  
 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
 arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472  
 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
 asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 2B (cont.)

1502	1532	
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC		
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn		
1562	1592	
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA		
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser		
1622	1652	
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT		
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp		
1682	1712	
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA		
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln		
1742	1772	
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT		
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile		
1802	1832	
AGG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT		
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe		
1862	1892	
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC		
thr tyr trp asn lys ala ser thr ser glu leu met asp phe thr ile ser glu val		
1922	1952	xxxxxxxxxxxxxxxxxxxxxx
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG		
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu		
1982	xxxxxxxxxx deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxx	
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA		
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly		
2042	2072	
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC		
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his		
2102	2132	
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT		
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala		
2162	2192	Deleted
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC		xxxx
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asp		
in HC2B		
xxx	2252	
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG		
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu		

FIG. 2B (cont.)

2282 2312  
 TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
 cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
 TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
 ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
 CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
 leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
 TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
 ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552  
 GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
 val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
 ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
 ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
 CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
 arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
 ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
 thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
 GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
 asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 Ixxxxxxxxxxxxxx Predicted  
 CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
 leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

[Additional and differential exon usage found at position 2927 consisting of 69 nucleotides. This entire sequence is found in Human CLASP-2D (KIAA1058) and not other isoforms of CLASP-2. It has a sequence of: AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCCACAGCCATAGCGCCTGCCAGGGAGGCCGGGGAGI]

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx!  
 TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
 tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
 GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
 gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

FIG. 2B (cont.)

3002           xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Sequence deleted in CLASP-2E xxxxx  
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 xxxxxxxxxxxxxxxxx 3092  
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT  
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

Additional and differential exon usage found at position 3153. The entire sequence below is found in Human CLASP-2D. Underlined sequence is found in Human CLASP-2B, 2C and 2E.

TGAGAGGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCAT  
GCACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGCGCAATACCAGTTT  
ACAGACAGTGAAACAGATGTGGAGGGATT]



3122           3155  
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT  
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182           3212  
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242           3272  
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC  
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302           3332  
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362           3392  
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC  
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422           3452  
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482           3512  
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC  
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys arg ile

Two nucleotide deletion (nts 358b and 3587) found in Human CLASP-2C

3542           3572           xxxx  
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG  
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

FIG. 2B (cont.)

3602	3632
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA	
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys	
3662	3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT	
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr	
3722	3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG	
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu	
3782	3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA	
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu	
3842	3872
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA	
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu	

□ Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

38902 3932  
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992  
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 Ixxxx PBM xxxx I  
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser val val STP

4082 4112  
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172  
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232  
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292  
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352  
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412  
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 4472

FIG. 2B (cont.)

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA  
4502 4532  
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA  
4562 4592  
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT  
4622 4652  
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC  
4682 4712  
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA  
4742 4772  
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC  
4802  
TTT ACT

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FIG. 2B (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCATCTGGAAATCTTGACAAAAATGCCAGATTTCTGCCATCTACAGGCAAGACAGCAAT
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTCGGAAACCTGAGAAGATG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCTAAGCTCCCAGTGATTTAGGCAATCTAGACATTACAATTGATAATGTTCCCTCAGAC
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTCCCTAATTATGTTAATTCATCATACTACATTCCCACAAAACAATTGAAACCTGCAGTAAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ACTCCCATCACGTTGAAGTGGAGGAATTGTGCCCTGCATACCAAAACACACTCAGCCT
HC2E	-----
HC2F	-----

FIG. 3A

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TACACCATCTACACCAATCACCTTACGTTATCCTAAGTACTGAAATACGACAGTCAG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTCTTTGCCAAGGCTAGAAATATTGCGATTGCATTGAATTCAAAGATTAGATGAG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GAAGACTCTCAGCCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTCACAAGA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTTTACACCATCACCAAAACCCAGAATTATGATGAGATTAAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCGCCTTGCTGCAGTTACACCATCACCAAAACCCAGAATTATGATGAGATTAAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATAGAGTTGCCACTCAGCTGCATGAAAGCACCACTGTTGCTCACATTCTCCATGTC
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATAGAGTTGCCACTCAGCTGCATGAAAGCACCACTGTTGCTCACATTCTCCATGTC
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCTGTGACAACCTCAAGTAAAGGAAGCAGCAAGAAGAGGGATGTCGTTGAAACCCAAGTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTACAAGCGAGCAGCACATC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTACAAGCGAGCAGCACATC
HC2E	-----
HC2F	-----
HC2A	CCGGTCTCGCGAACCTCCTCGGGCTATCTGGCTACCAAGAGCTTGGATGGCAGG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCGGTCTCGCGAACCTCCTCGGGCTATCTGGCTACCAGGAGCTTGGATGGCAGG
HC2E	-----
HC2F	-----
HC2A	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAATTCCACT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAATTCCACT
HC2E	-----
HC2F	-----
HC2A	CATCTGGTTCTACAGTGTATACTCAGGATCAGCATTACATAATTTCAGTACTGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATCTGGTTCTACAGTGTATACTCAGGATCAGCATTACATAATTTCAGTACTGT
HC2E	-----
HC2F	-----
HC2A	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTGTAAAGTACCTTAAGAGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTGTAAAGTACCTTAAGAGT
HC2E	-----
HC2F	-----
HC2A	CTGCATGCGATGGAAGGCCACGTGATGATGCCCTTGCCCACTATCCTAAACCAGCTG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CTGCATGCGATGGAAGGCCACGTGATGATGCCCTTGCCCACTATCCTAAACCAGCTG
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	TTCCGAGTCCTCACCAAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2-80	-----
HC2B	TTCCGAGTCCTCACCAAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2C	-----
HC2D-KIAA1058	TTCCGAGTCCTCACCAAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2E	TTCCGAGTCCTCACCAAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2F	-----
HC2A	ATTCATGTGGTTGCCAGTGCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2-80	-----
HC2B	ATTCATGTGGTTGCCAGTGCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2C	-----
HC2D-KIAA1058	ATTCATGTGGTTGCCAGTGCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2E	ATTCATGTGGTTGCCAGTGCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2F	-----
HC2A	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATAACAAGACAGTCATGAAGAA
HC2-80	-----
HC2B	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATAACAAGACAGTCATGAAGAA
HC2C	-----
HC2D-KIAA1058	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATAACAAGACAGTCATGAAGAA
HC2E	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATAACAAGACAGTCATGAAGAA
HC2F	-----
HC2A	CTGACCAATCCATGACCACGATTCTCAAGCCTCTGCCATTTCCTCACCAAGCAACAAA
HC2-80	-----
HC2B	CTGACCAATCCATGACCACGATTCTCAAGCCTCTGCCATTTCCTCACCAAGCAACAAA
HC2C	-----
HC2D-KIAA1058	CTGACCAATCCATGACCACGATTCTCAAGCCTCTGCCATTTCCTCACCAAGCAACAAA
HC2E	CTGACCAATCCATGACCACGATTCTCAAGCCTCTGCCATTTCCTCACCAAGCAACAAA
HC2F	-----
HC2A	CTACTGAGGTACTCATGGTTTTCTTGATGTACTGATCAAATCTATGGCTCAGCATTG
HC2-80	-----
HC2B	CTACTGAGGTACTCATGGTTTTCTTGATGTACTGATCAAATCTATGGCTCAGCATTG
HC2C	-----
HC2D-KIAA1058	CTACTGAAGTACTCATGGTTTTCTTGATGTACTGATCAAATCTATGGCTCAGCATTG
HC2E	CTACTGAGGTACTCATGGTTTTCTTGATGTACTGATCAAATCTATGGCTCAGCATTG
HC2F	-----
HC2A	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2-80	-----
HC2B	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2C	-----
HC2D-KIAA1058	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2E	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2F	-----

FIG. 3A (cont.)

HC2A	GCAGCGGAAACCGTTGAAATATGCTGATGCCACACATCACTCAGAAGTTGGAGATAAT
HC2-80	-----
HC2B	GCAGCGGAAACCGTTGAAATATGCTGATGCCACACATCACTCAGAAGTTGGAGATAAT
HC2C	-----
HC2D-KIAA1058	GCAGTGGAAACCGTTGAAATATGCTGATGCCACACATCACTCAGAAGTTCGAGATAAT
HC2E	GCAGCGGAAACCGTTGAAATATGCTGATGCCACACATCACTCAGAAGTTGGAGATAAT
HC2F	-----
HC2A	CCAGAGGCATCTAAGAACCGAATCATAGCCTGCTGTCTCATCAAGAGATGTTCACCC
HC2-80	-----
HC2B	CCAGAGGCATCTAAGAACCGAATCATAGCCTGCTGTCTCATCAAGAGATGTTCACCC
HC2C	-----
HC2D-KIAA1058	CCAGAGGCATCTAAGAACCGAATCATAGCCTGCTGTCTCATCAAGAGATGTTCACCC
HC2E	CCAGAGGCATCTAAGAACCGAATCATAGCCTGCTGTCTCATCAAGAGATGTTCACCC
HC2F	-----
HC2A	TTCATGGACAGGGCTTGCTTCAAGCAGATCAACAACTACATTAGCTTTGCTCCT
HC2-80	-----
HC2B	TTCATGGACAGGGCTTGCTTCAAGCAGATCAACAACTACATTAGCTTTGCTCCT
HC2C	-----
HC2D-KIAA1058	TTCATGGACAGGGCTTGCTTCAAGCAGATCAACAACTACATTAGCTTTGCTCCT
HC2E	TTCATGGACAGGGCTTGCTTCAAGCAGATCAACAACTACATTAGCTTTGCTCCT
HC2F	-----
HC2A	GGAGACCCAAAGACCCCTTTGAATACAAGTTGAATTCTCCGTGTAGTGTGCAACCAT
HC2-80	-----
HC2B	GGAGACCCAAAGACCCCTTTGAATACAAGTTGAATTCTCCGTGTAGTGTGCAACCAT
HC2C	-----
HC2D-KIAA1058	GGAGACCCAAAGACCCCTTTGAATACAAGTTGAATTCTCCGTGTAGTGTGCAACCAT
HC2E	GGAGACCCAAAGACCCCTTTGAATACAAGTTGAATTCTCCGTGTAGTGTGCAACCAT
HC2F	-----
HC2A	GAACATTATATTCCGTTGAACCTACCAATGCCATTGGAAAAGGCAGGATTCAAAGATAAC
HC2-80	-----
HC2B	GAACATTATATTCCGTTGAACCTACCAATGCCATTGGAAAAGGCAGGATTCAAAGATAAC
HC2C	-----
HC2D-KIAA1058	GAACATTATATTCCGTTGAACCTACCAATGCCATTGGAAAAGGCAGGATTCAAAGATAAC
HC2E	GAACATTATATTCCGTTGAACCTACCAATGCCATTGGAAAAGGCAGGATTCAAAGATAAC
HC2F	-----
HC2A	CAAGACCTCCAGCTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTGGTG
HC2-80	-----
HC2B	TCCAGCTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTGGTG
HC2C	CAAGACCTCCAGCTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTGGTG
HC2D-KIAA1058	CAAGACCTCCAGCTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTGGTG
HC2E	CAAGACCTCCAGCTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTGGTG
HC2F	-----

FIG. 3A (cont.)

HC2A	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2-80	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2B	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2C	-----
HC2D-KIAA1058	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2E	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2F	-----
HC2A	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTGATGACAGATATGCTTCA
HC2-80	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTGATGACAGATATGCTTCA
HC2B	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTGATGACAGATATGCTTCA
HC2C	-----
HC2D-KIAA1058	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTGATGACAGATATGCTTCA
HC2E	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTGATGACAGATATGCTTCA
HC2F	-----
HC2A	AGGAGCCATCAGGCAAGGAAGCCACCCCTTACCTGCCTCTGTTGGTCTGCTGATTGAA
HC2-80	AGGAGCCATCAGGCAAGGAAGCCACCCCTTACCTGCCTCTGTTGGTCTGCTGATTGAA
HC2B	AGGAGCCATCAGGCAAGGAAGCCACCCCTTACCTGCCTCTGTTGGTCTGCTGATTGAA
HC2C	-----
HC2D-KIAA1058	AGGAGCCATCAGGCAAGGAAGCCACCCCTTACCTGCCTCTGTTGGTCTGCTGATTGAA
HC2E	AGGAGCCATCAGGCAAGGAAGCCACCCCTTACCTGCCTCTGTTGGTCTGCTGATTGAA
HC2F	-----
HC2A	AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCCTCCGTGAACGCGGGCATGACC
HC2-80	AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCCTCCGTGAACGCGGGCATGACC
HC2B	AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCCTCCGTGAACGCGGGCATGACC
HC2C	-----
HC2D-KIAA1058	AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCCTCCGTGAACGCGGGCATGACT
HC2E	AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCCTCCGTGAACGCGGGCATGACC
HC2F	-----
HC2A	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA
HC2-80	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA
HC2B	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA
HC2C	-----
HC2D-KIAA1058	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA
HC2E	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA
HC2F	-----
HC2A	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGCGCCATCTCCGGCATTGCTTCT
HC2-80	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGCGCCATCTCCGGCATTGCTTCT
HC2B	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGCGCCATCTCCGGCATTGCTTCT
HC2C	-----
HC2D-KIAA1058	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGCGCCATCTCCGGCATTGCTTCT
HC2E	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGCGCCATCTCCGGCATTGCTTCT
HC2F	-----

FIG. 3A (cont.)

HC2A	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT
HC2-80	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT
HC2B	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT
HC2C	-----
HC2D-KIAA1058	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT
HC2E	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT
HC2F	-----GCTGATTGAGAGGATCT
HC2A	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2-80	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2B	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2C	-----
HC2D-KIAA1058	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2E	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2F	CTCATAGCACAGATTGGTAACAGCCTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2A	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2-80	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2B	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2C	-----
HC2D-KIAA1058	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2E	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2F	CTGGATAAGCACCAACAAAGTAGCACATTGGAAATTCCGTGGTCGCTGTGATAAAACTT
HC2A	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2-80	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2B	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2C	-----
HC2D-KIAA1058	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2E	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2F	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTCTACATCTAAAGAGCATGTCT
HC2A	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2-80	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2B	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2C	-----
HC2D-KIAA1058	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2E	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2F	GATGATGCTTGTACATATTGAAACAAGGCTCAACATCTGAACCTATGGATTTTTT
HC2A	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG
HC2-80	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG
HC2B	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG
HC2C	-----
HC2D-KIAA1058	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG
HC2E	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG
HC2F	ACAATATCTGAAGTCTGCCTGCACCAGTCCAGTACATGGGAAGCGATACATAGCCAGG

Fig. 3A (cont.)

HC2A	AACCAGGAGGGTTGGGACCCATAGTCATGATCGAAAGTCTCAGACATTGCCTGTTCC
HC2-80	AACCAGGAGGGTTGGGACCCATAGTCATGATCGAAAGTCTCAGACATTGCCTGTTCC
HC2B	AACCAGGAGGGTTGGGACCCATAGTCATGATCGAAAGTCTCAGACATTGCCTGTTCC
HC2C	-----
HC2D-KIAA1058	-----AA-----
HC2E	AACCAGGAGGGTTGGGACCCATAGTCATGATCGAAAGTCTCAGACATTGCCTGTTCC
HC2F	-----TGTGA-----GAAAG-----ATATCAAGTGT-----
 2000	
HC2A	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGCAGCCTGGATAACTCT
HC2-80	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGCAGCCTGGATAACTCT
HC2B	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGCAGCCTGGATAACTCT
HC2C	-----
HC2D-KIAA1058	-----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGCAGCCTGGATAACTCT
HC2E	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGCAGCCTGGATAACTCT
HC2F	-----GCTTGGAA-----
 2000	
HC2A	CTCACTTTAACCAACAGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2-80	CTCACTTTAACCAACAGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2B	CTCACTTTAACCAACAGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2C	-----
HC2D-KIAA1058	CTCACTTTAACCAACAGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2E	CTCACTTTAACCAACAGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2F	-----TTTCTGTAGACAATGGCTATGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
 2000	
HC2A	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
HC2-80	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
HC2B	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
HC2C	-----
HC2D-KIAA1058	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
HC2E	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
HC2F	GAAGCCAACATTGCTACTGAGGTTGCCTGACAGCTCTGGACACGCTTCTATTACA
 2000	
HC2A	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
HC2-80	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
HC2B	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
HC2C	-----
HC2D-KIAA1058	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
HC2E	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
HC2F	TTGGCGTTAACGACAGCTCTGGCCGACCATGGACATAATCCTCTCATGAAAAAGTT
 2000	
HC2A	TTTGATGTCTACCTGTGTTCTCAAAAACATCAGTCTGAAACGGCTTAAAAATGTC
HC2-80	TTTGATGTCTACCTGTGTTCTCAAAAACATCAGTCTGAAACGGCTTAAAAATGTC
HC2B	TTTGATGTCTACCTGTGTTCTCAAAAACATCAGTCTGAAACGGCTTAAAAATGTC
HC2C	-----
HC2D-KIAA1058	TTTGATGTCTACCTGTGTTCTCAAAAACATCAGTCTGAAACGGCTTAAAAATGTC
HC2E	TTTGATGTCTACCTGTGTTCTCAAAAACATCAGTCTGAAACGGCTTAAAAATGTC
HC2F	A-----

Fig. 3A (cont.)

HC2A	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2-80	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2B	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2C	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2D-KIAA1058	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2E	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
HC2F	TTCACTGCCTTAAGGTCTTAATTATAAGTTCCCTAACATTCTATGAAGGGAGAGCG
<hr/>	
HC2A	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2-80	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2B	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2C	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2D-KIAA1058	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2E	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
HC2F	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC
<hr/>	
HC2A	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2-80	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2B	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2C	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2D-KIAA1058	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2E	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
HC2F	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACTTGATTACACT
<hr/>	
HC2A	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2-80	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2B	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2C	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2D-KIAA1058	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2E	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2F	GGAAAGAAGTCCTTGTCCGGACACATTGCAAGTCATCATATCTGTCAGCCAGCTGATA
<hr/>	
HC2A	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2-80	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2B	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2C	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2D-KIAA1058	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2E	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
HC2F	GCAGACGTGTTGGCATTGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAAC
<hr/>	
HC2A	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2-80	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2B	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2C	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2D-KIAA1058	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2E	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2F	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA

FIG. 3A (cont.)

HC2A	ACCAAAAGGATA CGCACGGT GCTAATGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2-80	ACCAAAAGGATA CGCACGGT GCTAATGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2B	ACCAAAAGGATA CGCACGGT GCTAATGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2C	-----
HC2D-KIAA1058	ACCAAAAGGATA CGCACGGT GCTAATGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2E	ACCAAAAGGATA CGCACGGT GCTAATGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2F	-----
HC2A	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCAAATCCTATGCCAGCACGCCGAG
HC2-80	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCAAATCCTATGCCAGCACGCCGAG
HC2B	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCAAATCCTATGCCAGCACGCCGAG
HC2C	-----
HC2D-KIAA1058	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCAAATCCTATGCCAGCACGCCGAG
HC2E	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCAAATCCTATGCCAGCACGCCGAG
HC2F	-----
HC2A	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2-80	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2B	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2C	-----
HC2D-KIAA1058	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2E	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2F	-----
HC2A	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2-80	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2B	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2C	-----
HC2D-KIAA1058	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2E	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2F	-----
HC2A	G-----
HC2-80	G-----
HC2B	G-----
HC2C	-----
HC2D-KIAA1058	GAAGCAGTCCAGTGGAGCCGCCCTCTCCCCCACAGCCATAGCGCCTGCCTGAGGAGG
HC2E	G-----
HC2F	-----
HC2A	-----GCGTGTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2-80	-----GCGTGTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2B	-----GCGTGTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2C	-----GTTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2D-KIAA1058	AGCCGGGAGGCGTGTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2E	-----GCGTGTAGACAAGGATGCACCGCCTCAGGGTATTACCCAAACATC
HC2F	-----

FIG. 3A (cont.)

HC2A	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2-80	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2B	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2C	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2D-KIAA1058	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2E	GACGAGGAGGCCTCCATGATGGAAGACGTGGGATGCAGGATGTCCATTCAACGAGGAT
HC2F	-----
HC2A	GTGCTGATGGAGCTCCTTGAGCAGTGCAGATGGACTCTGAAAGCCGAGCGCTACGAG
HC2-80	GTGCTGATGGAGCTCCTTGAGCAGTGCAGATGGACTCTGAAAGCCGAGCGCTACGAG
HC2B	GTGCTGATGGAGCTCCTTGAGCAGTGCAGATGGACTCTGAAAGCCGAGCGCTACGAG
HC2C	GTGCTGATGGAGCTCCTTGAGCAGTGCAGATGGACTCTGAAAGCCGAGCGCTACGAG
HC2D-KIAA1058	GTGCTGATGGAGCTCCTTGAGCAGTGCAGATGGACTCTGAAAGCCGAGCGCTACGAG
HC2E	-----AAGCCGAGCGCTACGAG
HC2F	-----
HC2A	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2-80	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2B	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2C	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2D-KIAA1058	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2E	CTCATGCCGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	AGGCTGGCCCCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCTG
HC2C	AGGCTGGCCCCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCTG
HC2D-KIAA1058	AGGCTGGCCCCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCTG
HC2E	AGGCTGGCCCCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCTG
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	CACTCGGGCCGCAGGCTCTGGGACCTACTTCCGGTAGCCTTCTCGGGCAGG-----
HC2C	CACTCGGGCCGCAGGCTCTGGGACCTACTTCCGGTAGCCTTCTCGGGCAGG-----
HC2D-KIAA1058	CACTCGGGCCGCAGGCTCTGGGACCTACTTCCGGTAGCCTTCTCGGGCAGG-----
HC2E	CACTCGGGCCGCAGGCTCTGGGACCTACTTCCGGTAGCCTTCTCGGGCAGG-----
HC2F	-----
HC2A	-----CTTTGAAGATGAAGATGGA
HC2-80	-----CTTTGAAGATGAAGATGGA
HC2B	-----GATTCTTGAAAGATGAAGATGGA
HC2C	-----GATTCTTGAAAGATGAAGATGGA
HC2D-KIAA1058	CAATACCACTTACAGACAGTGAACAGATGTGGAGGGATTCTTGAAAGATGAAGATGGA
HC2E	-----GATTCTTGAAAGATGAAGATGGA
HC2F	-----

FIG. 3A (cont.)

HC2A	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2-80	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2B	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2C	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2D-KIAA1058	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2E	AAGGAGTATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTCTCAGAGACTC
HC2F	-----
HC2A	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2-80	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2B	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2C	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGACACAGGATTCTGGC
HC2D-KIAA1058	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2E	CTTAAACTGTACTCGGATAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2F	-----
HC2A	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2-80	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2B	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2C	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2D-KIAA1058	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC
HC2E	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2F	-----
HC2A	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2-80	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2B	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2C	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2D-KIAA1058	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2E	CCCTTCTTGACAAAAAGAGTTGCAAGAAAGGAAACAGAGTTGAGAGATCCCACAAC
HC2F	-----
HC2A	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2-80	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2B	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2C	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2D-KIAA1058	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2E	ATCCGCCGCTTCATGTTGAGATGCCATTACGCAGACCGGAAAGAGGCAGGGCGGGGTG
HC2F	-----
HC2A	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2-80	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2B	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2C	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2D-KIAA1058	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2E	GAAGAGCAGTGCACCGGGCACCACCTGACAGCCATACACTGCTCCCTATGTGAAG
HC2F	-----

Fig. 3A (cont.)

HC2A	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2-80	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2B	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2C	AAGCGCATCCCTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT
HC2D-KIAA1058	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2E	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2F	-----
HC2A	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2-80	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2B	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2C	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2D-KIAA1058	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2E	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2F	-----
HC2A	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2-80	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2B	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2C	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2D-KIAA1058	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2E	ATGATCAAACAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCA
HC2F	-----
HC2A	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2-80	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2B	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2C	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2D-KIAA1058	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2E	CTAGCATATGCGCGAGCTTCTTAGATGATAACAAACACAAAGCGATATCCTGACAATAAA
HC2F	-----
HC2A	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2-80	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2B	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2C	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2D-KIAA1058	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2E	GTGAAGCTGTTAAGGAAGTTTCAGGCAATTGTGGAAGCTTGCCTAGCG
HC2F	-----
HC2A	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2-80	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2B	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2C	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2D-KIAA1058	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2E	GTAAACGAACGTCTGATTAAAGAACGAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2F	-----

FIG. 3A (cont.)

HC2A	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAG-----	ATCTGCC
HC2-80	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAG-----	ATCTGCC
HC2B	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAG-----	ATCTGCC
HC2C	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAG-----	ATCTGCC
HC2D-KIAA1058	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAGCTGGATGATCTGCC	
HC2E	TACAGGGAAATGGCGAAGGAGCTTCTGAAATCATGCATGAGCAG-----	ATCTGCC
HC2F	-----	
HC2A	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2-80	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2B	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2C	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2D-KIAA1058	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2E	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTCACATCTCAACGCCATCAGTG	
HC2F	-----	
HC2A	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2-80	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2B	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2C	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2D-KIAA1058	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2E	GGACTCCAACAAGCACAATGGTCACGGGATGACCAGCTCGTCTCGGTCGTGATTAC	
HC2F	-----	
HC2A	ATCTCATGGCCCGTGTGGGGACTTGCTTGTCAATTGCAAACTCAGGATGCTTCAA	
HC2-80	ATCTCATGGCCCGTGTGGGGACTTGCTTGTCAATTGCAAACTCAGGATGCTTCAA	
HC2B	-----	
HC2C	-----	
HC2D-KIAA1058	ATCTCATGGCCCGTGTGGGGACTTGCTTGTCAATTGCAAACTCAGGATGCTTCAA	
HC2E	-----	
HC2F	-----	
HC2A	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA	
HC2-80	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA	
HC2B	-----	
HC2C	-----	
HC2D-KIAA1058	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA-GGGGAAGGGGAGAGAAAGGAAA	
HC2E	-----	
HC2F	-----	
HC2A	TAAAGAACACGTTATTCCTAACAGACTTCTATAGGAGTTGTAAGAACGGTCACATAT	
HC2-80	TAAAGAACACGTTATTCCTAACAGACTTCTATAGGAGTTGTAAGAACGGTCACATAT	
HC2B	-----	
HC2C	-----	
HC2D-KIAA1058	TAAAGAACACGTTATTCCTAACAGACTTCTATAGGAGTTGTAAGAACGGTCACATAT	
HC2E	-----	
HC2F	-----	

FIG. 3A (cont.)

HC2A	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTATTGTGTCTTAACAAAGGTGTGGTA
HC2-80	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTATTGTGTCTTAACAAAGGTGTGGTA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTATTGTGTCTTAACAAAGGTGTGGTA
HC2E	-----
HC2F	-----
HC2A	GACACTCTTGAGCTGGACTTAGATTATTCTTCCTGCAGAGTAGTGTAGAATAGATG
HC2-80	GACACTCTTGAGCTGGACTTAGATTATTCTTCCTGCAGAGTAGTGTAGAATAGATG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GACACTCTTGAGCTGGACTTAGATTATTCTTCCTGCAGAGTAGTGTAGAATAGATG
HC2E	-----
HC2F	-----
HC2A	GCCTACAGAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2-80	GCCTACAGAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTACAGAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2E	-----
HC2F	-----
HC2A	GCCTGGGGGACCTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA
HC2-80	GCCTGGGGGACCTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTGGGGGACCTTTGCCTCGAGGCTGAGCTGGAAAATCTGAAAATATTTT-----T
HC2E	-----
HC2F	-----
HC2A	CTTACTAGTTTGTCTAGGAGTATGTTATGACTAGGATTGTGCTATTATCTCATTCA
HC2-80	CTTACTAGTTTGTCTAGGAGTATGTTATGACTAGGATTGTGCTATTATCTCATTCA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTCCTGTGGCACATTCAAGGTTGAATACAAGAACTATTTGTGACTAGTTTGATGAC
HC2E	-----
HC2F	-----
HC2A	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAAATCCGCTACTGG
HC2-80	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAAATCCGCTACTGG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CTAAGGGAACTGACCATTGTAATTTGTACCAAGTGAACCAGGAGATTAGTGTCTTTAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	CTTCAAGTCAGAACTTGTCTTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80	CTTCAAGTCAGAACTTGTCTTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATTCAATTCCCTGCATTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTAAACT
HC2E	-----
HC2F	-----
HC2A	TTCTACATTTAATACTCACATGGGCTTATGCATTAAGTTAATTGTGATAAATTTGTG
HC2-80	TTCTACATTTAATACTCACATGGGCTTATGCATTAAGTTAATTGTGATAAATTTGTG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTCAAGCAGTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E	-----
HC2F	-----
HC2A	CTGGTCCAGTATATGCAATACACTTTAATGGTTATTCTTGTCAAAAAATGTGCAATAT
HC2-80	CTGGTCCAGTATATGCAATACACTTTAATGGTTATTCTTGTCAAAAAATGTGCAATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E	-----
HC2F	-----
HC2A	GGAGATGTATACAAGTCTTACT-----
HC2-80	GGAGATGTATACAAGTCTTACT-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATATATGTATTACATTCTACATTTAATACTCACATGGGCTTATGCATTAAGTTAAT
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGTGATAAATTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTATTCTGTACA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAAATGTGCAATATGGAGATGTACAGTCTTACTATATTAGGTTATAAACAGTTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAGAATTCATCCTTGC <del>AAA</del> ATGGTGGAGTATGTAATTGGTAAATCATAAAATCCTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATTTCTTTAAGACATTAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTAGTAATTTATTTGGGAAAATAAAGGTTTTAATTAACTGGAATCACTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCCTGCTGTAATTAAACATTCTGTACCA <del>CATCTG</del> TATTA <del>AAA</del> AGACATTGCTGACC
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
ASGNLDKNARFSAIYRQDSNKLNSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD  
HC2E  
HC2F

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ  
HC2E  
HC2F

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFRSAFAAVLHHHQNPFYDEIK  
HC2E  
HC2F

HC2A  
HC2A-80  
HC2B  
HC2C  
IELPTQLHEKHHLLTFFHVSCDNSSKGSTKKRDVVEIQVGYSWLPLLKDGRVVTSEQHI  
HC2D  
HC2E  
HC2F

HC2A  
HC2A-80  
HC2B  
HC2C  
PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC  
HC2D  
HC2E  
HC2F

HC2A  
HC2A-80  
HC2B  
HC2C  
QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI  
HC2D  
HC2E  
HC2F  
AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI  
QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI  
AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI

FIG. 3B

HC2A	IHVVAQCHEEGLESHRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2A-80	-----
HC2B	IHVVAQCHEEGLESHRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2C	-----
HC2D	IHVVAQCHEEGLESHRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2E	IHVVAQCHEEGLESHRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2F	-----
HC2A	LLRYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPASYHAAETVVNMLMPHITQKFGDN
HC2A-80	-----
HC2B	LLRYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPASYHAAETVVNMLMPHITQKFGDN
HC2C	-----
HC2D	LLKYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPASYHAAETVVNMLMPHITQKFRDN
HC2E	LLRYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPASYHAAETVVNMLMPHITQKFGDN
HC2F	-----
HC2A	PEASKNAHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2A-80	-----
HC2B	PEASKNAHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2C	-----
HC2D	PEASKNAHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2E	PEASKNAHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2F	-----
HC2A	EHYIPLNLPMPPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVTALQEREVRLI
HC2A-80	-----QLDYSLTDEFCRNHFLVGLLLREVTALQEREVRLI
HC2B	EHYIPLNLPMPPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVTALQEREVRLI
HC2C	-----
HC2D	EHYIPLNLPMPPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVTALQEREVRLI
HC2E	EHYIPLNLPMPPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVTALQEREVRLI
HC2F	-----
HC2A	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2A-80	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2B	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2C	-----
HC2D	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2E	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2F	-----
HC2A	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIAСПTTSTPNINSVRNADSRGS
HC2A-80	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIAСПTTSTPNINSVRNADSRGS
HC2B	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIAСПTTSTPNINSVRNADSRGS
HC2C	-----
HC2D	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIAСПTTSTPNINSVRNADSRGS
HC2E	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIAСПTTSTPNINSVRNADSRGS
HC2F	-----ADSRGS

FIG. 3B (cont.)

HC2A	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A-80	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2B	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2C	-----
HC2D	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2E	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2F	LISTDSGNSLPERNSEKNSLDKHQQSSTLGNNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2A-80	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2B	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2C	-----
HC2D	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2E	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2F	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIAS-----VR--KISSVLGIS
HC2A	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A-80	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2B	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2C	-----
HC2D	---TGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2E	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2F	V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A	LAFKNQLLADHGNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2A-80	LAFKNQLLADHGNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2B	LAFK--LLADHGNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2C	-----
HC2D	LAFKNQLLADHGNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2E	LAFKNQLLADHGNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2F	LAFKNQLLADHGNPLMKK-----
HC2A	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQI
HC2A-80	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQI
HC2B	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQI
HC2C	-----
HC2D	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQI
HC2E	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQI
HC2F	-----
HC2A	ADVVGIGETRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMAQMKEHEND
HC2A-80	ADVVGIGETRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMAQMKEHEND
HC2B	ADVVGIGETRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMAQMKEHEND
HC2C	-----
HC2D	ADVVGIGGTRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMAQMKEHEND
HC2E	ADVVGIGETRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMAQMKEHEND
HC2F	-----

FIG. 3B (cont.)

HC2A	PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGLSEAAMCYVHTALVAEYLTRK
HC2A-80	PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGLSEAAMCYVHTALVAEYLTRK
HC2B	PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGLSEAAMCYVHTALVAEYLTRK
HC2C	-----
HC2D	PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGLSEAAMCYVHTALVAEYLTRK
HC2E	PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGLSEAAMCYVHTALVAEYLTRK
HC2F	-----
HC2A	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2A-80	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2B	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2C	-----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2D	EAVQWEPLLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2E	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2F	-----
HC2A	DVLMELLEQCADGLWKAERYELIADIYKLIIPIFYEKRR-----
HC2A-80	DVLMELLEQCADGLWKAERYELIADIYKLIIPIFYEKRR-----
HC2B	DVLMELLEQCADGLWKAERYELIADIYKLIIPIFYEKRRDFERLAHLYDTLHRAYSK
HC2C	DVLMELLEQCADGLWKAERYELIADIYKLIIPIFYEKRRDFERLAHLYDTLHRAYSK
HC2D	DVLMELLEQCADGLWKAERYELIADIYKLIIPIFYEKRRDFERLAHLYDTLHRAYSK
HC2E	-----KAERYELIADIYKLIIPIFYEKRRDFERLAHLYDTLHRAYSK
HC2F	-----
HC2A	-----DFFEDEDGKEYIYKEPKLTPNSE
HC2A-80	-----DFFEDEDGKEYIYKEPKLTPNSE
HC2B	VTEVMHSGRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPNSE
HC2C	VTEVMHSGRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPNSE
HC2D	VTEVMHSGRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPNSE
HC2E	VTEVMHSGRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPNSE
HC2F	-----
HC2A	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2A-80	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2B	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2C	ISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2D	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2E	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLSKYAYIQVTHVIPFFDEKELQERKTEF
HC2F	-----
HC2A	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2A-80	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2B	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2C	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2D	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2E	ERSHNIRRPFEMPFTQTGKRQGGVEECKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2F	-----

FIG. 5B (cont.)

HC2A IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR  
HC2A-80 IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR  
HC2B IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR  
HC2C IEVHZ-----  
HC2D IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR  
HC2E IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR  
HC2F -----

HC2A YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ  
HC2A-80 YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ  
HC2B YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ  
HC2C -----  
HC2D YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ  
HC2E YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ  
HC2F -----

HC2A ICPLEEKTSVLPNSLHI FNAISGTPSTMVHGMTSSSSVVZ-----  
HC2A-80 ICPLEEKTSVLPNSLHI FNAISGTPSTMVHGMTSSSSVVZ-----  
HC2B ICPLEEKTSVLPNSLHI FNAISGTPSTMVHGMTSSSSVVZ-----  
HC2C -----  
HC2D LG-----  
HC2E ICPLEEKTSVLPNSLHI FNAISGTPSTMVHGMTSSSSVVZ-----  
HC2F -----

FIG. 3B (cont.)

PBL

lung

placenta

sm intestine

liver

kidney

spleen

thymus

colon

skel muscle

heart

brain

FIG. 4A

~ 7.5 kb —

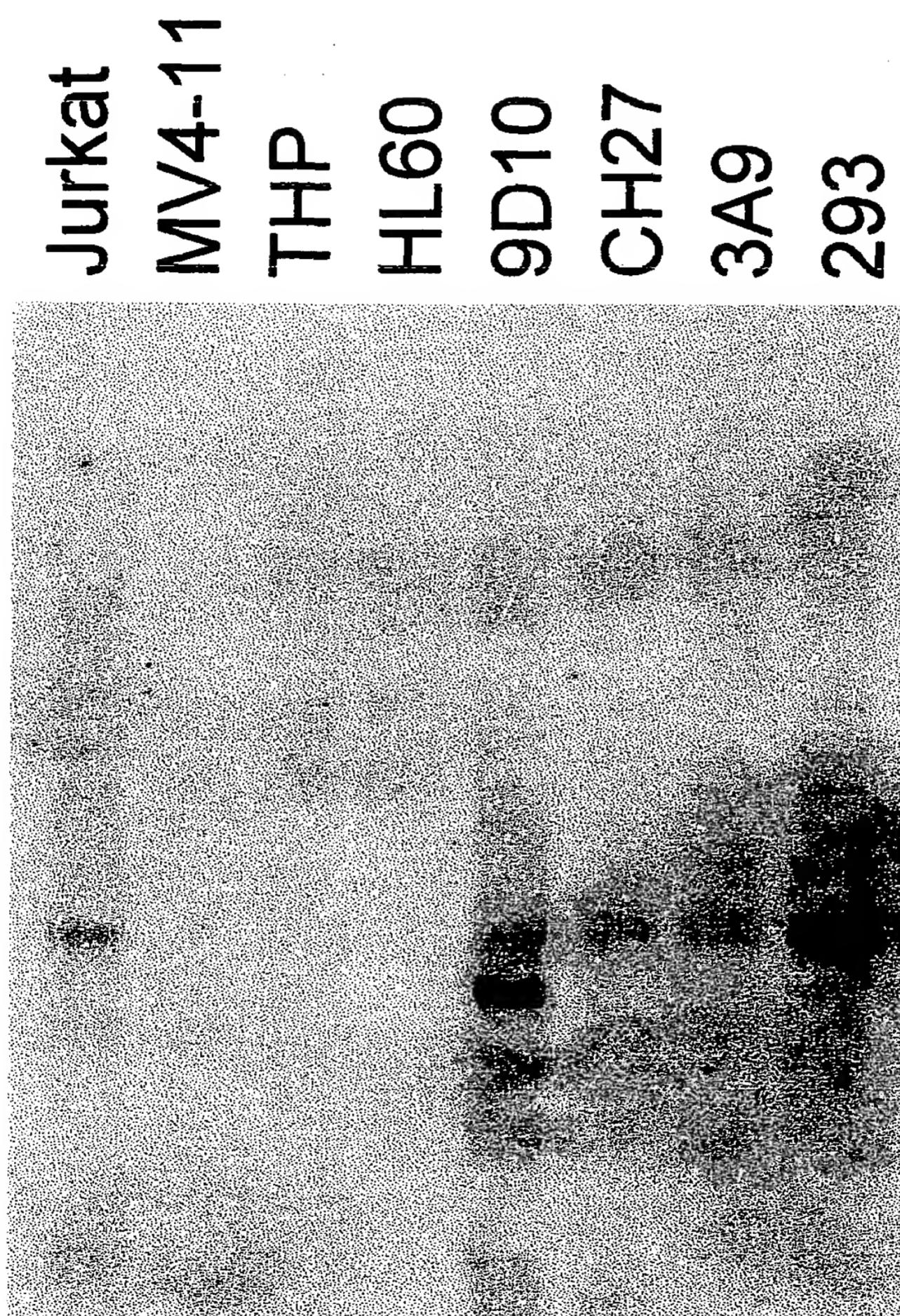


FIG. 4B

HC2A	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQLKCIFYGRPGGPVFTRSAFAAVLHHHQNPFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLLTFHVSCDNSSKGSTKKRDVVEQVGVYWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLLTFHVSCDNSSKGSTKKRDVVEQVGVYWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	-----NRSRSLNSNPDISGTPSPDDEVRSIIGSKGLDRSNWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 5A

HC2A	IIHVAQCHEE-----SHLRSYVKYAYKAEPYVASEYKTVHEELT-----TTILKPSADFLTSN
KIAA	IIHVAQCHEE-----SHLRSYVKYAYKAEPYVASEYKTVHEELT-----TTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLL-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCVG--SVR---E
HC5	-----
Cadherin Cleavage	
HC2A	KLLRYSWFFF DV LIKSMAQHLIENS KV KLLRNQRFPAS YHAAE TVVNMLMPHITQKFGD
KIAA	KLLKYSWFFF DV LIKSMAQHLIENS KV KLLRNQRFPAS YHAAE TVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFF EI IA KSMA T YLLEEN KIKLTHGQRFPKAYH HALH SFLA IT- IVE S QYAE
HC1	HVLKHSWFFF AI IL KSMAQHLIDTNKIQ LPRPQRFPESYQNE LDNL VMLV SDHVIW KYKD
HC3	SALQQAWFF FELMV KSMV HHL YFNDKLEAPR KSR FPER FMDDIA ALV STI AS DIVS RFQK
HC5	-----
HC2A	NPEASKNAHSLAVFIKRCFTFMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNAHSLAVFIKRCFTFMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVN YSLASFLKCCLTLMDRGFVFNLIN--DYIS--GFSPKDPKVLA EYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN--NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTSLAFFFLNDLLSVM DRGFVFS LIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL---EYLSDEY
HC1	QEVCQHEHFIPLCLPIRSANI PDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHEHYVTLNLPCSLLTPPASPSVSSAT SQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS--SQNSSSCSSFQDQKIASMFDRTSRVPA
HC2A	CRNHFLVGLL REVGTALQE FRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLL REVGTALQE FRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLL RETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1	CRKHFLIGILL REVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGLVLTELAVILD PDAEGLFGLHKKV INMVHNLLSSHDSDPRYSDPQIKARVAM
HC5	SSTS-SPGLLFTELAA ALDAE GEGI SEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAA
HC2A	LYLPLFGLLIENVQRINV RDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINV RDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPFVG LLENIQR LAGRDTLYSCAAMPNSASRDEFPCG---FTSP--AN--RGSL S
HC1	LYMPLYGMLLDNM PRIY LKDLYPFTVN TSNQGSR DDLSTNGGFQSQTAIKHANSV DTSFS
HC3	LYLPLIGIIMETVPQLYDFTE THNQRGRPICIATDDYESE-----SG--SMIS
HC5	LYLPLVGIILDALPQLCDF TVADTRRYR---TSGSDEEQE-----GA---GAIT
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDGSNSLPERNSEKNSLDKHQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDGSNSLPERNSEKNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTGEN----TRQS
HC1	KDV LNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIA GTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSL PYKQYN-----

FIG. 5A (cont.)

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISETLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLLICLLWVLKN-ADETVLQKWFDTLSVLQLNRLLDLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRSGVM
HC1	QNFRYLGKRNIIRKIAAAAF--KVFQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSREGHK
HC3	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAAILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTEADI FHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK--NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGR
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMAKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3	LIILDITLEIVVQTVS--VTE--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRLIA
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAF CYEVLKCCCTS KISS TRNEAS ALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHSRSTQTEAS ALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5	KFGDLLFEEEVEQCFDLCHQVLHHCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQLIADVVGIGETRFQQQLSIIINNCANSDRLIKHTSFSSDVKDLTKRIRTVM
KIAA	LQVIISVSQLIADVVGIGGTRFQQQLSIIINNCANSDRLIKHTSFSSDVKDLTKRIRTVM
rat	LQVIISLSQLIADVVGIGGTRFQQQLSIIINNCANSDRLIKHTSFSSDVKDLTKRIRTVM
HC4	LQIIIAVSQLIADVVALSGGSRFQESLFIIINNFANSDRPMLARAFPAEVKDLTKRIRTVM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAAEVKDLTKRIRTVM
HC3	MQVPMSSLVGTSQLNFNEEFLRRSLKTIILTYAEEDLELRETTFPDQVQDLVFNLHMLS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLNLNSILY

FIG. 5A (cont.)

HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKGDLSEAAMCYVHV  
 KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKGDLSEAAMCYVHV  
 rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKGDLSEAAMCYVHV  
 HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMARIHVKGDFSEAAMCYVHV  
 HC1 ATAQMKEHEKDPEMLVDLQSLANSYASTPELRRTWLES MAKIHARNGDLSEAAMCYIHI  
 HC3 DTVKMKEHQEDPEMLIDL MYRIAKGYQTSPDLRLTWLQN MAGKHSERSN HAEAAQCLVHS  
 HC5 DTVKMREFQEDPEMLMDL MYRIAKSYQAS PDLRLTWLQN MAEKHTKKCYTEAAMCLVHA

SH3

HC2A TALVAEYL	TRKGV-----	FRQGCTAFRVITPN
KIAA TALVAEYL	TRKEA-----	VQWE PPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat TALVAEYL	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4 AALVAEFL	HRKKL-----	FPNGCSAFKKITPN
HC1 AALIAEYL	KRKGYWKVEKIC	TASLLSEDTHPCDSNSLLTPSGGSMFSMGWPAFLSITPN
HC3 AALVAEYL	SMLED-----	RKYLPVGCVTFQNISSN
HC5 AALVAEYL	SMLED-----	HSYLPVGSVSFQNISSN

IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  
 IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  
 IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERL RAGLLTSINSSSP  
 IDEEGAMKEDAGMM-----VHYSEEVLLLEQCVNGLWKAERYEIISEISKLIGPI  
 IKEEGA AKEDSGMHD-----TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV  
 VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASF SMAGMYEAVNEVYKVLIP  
 VLEESVVSEDTLSPDEDGVCA GQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP

ITAM ITAM ITAM ITAM  
 HC2A YEKRRD-----  
 KIAA YEKRRDFERLAHLYDTLH RAYSKVTEVMHSGRLLGTYFRW AFFGQAAQYQFTDSETDVE  
 rat SMKSGGTLETTHLYDTLH RPYSKVTEVITR-----A-----AGSWD LLLPGGLFGQ  
 HC4 YENRREFENLTQVYRTLH GAYTKILEVMHTKRLLG-----TFFRVAFYGQ  
 HC1 FEKQRDFKKLSDIYYDIHRSYLVKAEVVNSEKRLFG-----RYYRVAFYGQ  
 HC3 HEANRDAKKLSTIHGKLQEA FSKIVHQSTGWERMFG-----TYFRVGFYG-  
 HC5 LEAHREFRKLT LTHSKLQRAFDSIVNKDH--KRMFG-----TYFRVGFYGG-

ITAM ITAM  
 HC2A -FFEDEDGKEYIYKEPKL TPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKD LSKYA  
 KIAA GFFEDEDGKEYIYKEPKL TPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKD LSKYA  
 rat GFFEDEDGKEYIYKEPKL TPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKD LSKFA  
 HC4 SFEEEDGKEYIYKEPKL TGLSEISLRLV KLYGEKFGTENVKIIQDSDKVNAKELDPKYA  
 HC1 GFEEEEGKEYIYKEPKL TGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKD LDPKYA  
 HC3 TKFGDLDEQE FVYKEPAITKLAEI SHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA  
 HC5 SKFGDLDEQE FVYKEPAITKLPEI SHRLEAFYQ QFGAEFVEVIK DSTPVDKT KLD PNKA

ITAM  
 HC2A YIQVTHVIPFFDEKE LQERKTE FERSHNIIRRFM FEMPFTQTGKRQGGVEEQCKRRTILTA  
 KIAA YIQVTHVIPFFDEKE LQERKTE FERSHNIIRRFM FEMPFTQTGKRQGGVEEQCKRRTILTA  
 rat YIQVTHVTPFFDEKE LQERKTE FERCHNIIRRFM FEMPFTQTGKRQGGVEEQCKRRTILTA  
 HC4 HIQVTVVKPYFDDKELTERKTE FERNHNISRFVFEAPYTLSGKKQGCIEE QCKRRTILTT  
 HC1 YIQVTVTPFFEEKEIEDRKTD FEMHHNINRFVFTPFTLSGKKHGGVAE QCKRRTILTT  
 HC3 YIQITVVEPYFDTYEMKDRIT YFDKNYNLRRFMYCTPFTLDGRAH GELHEQFKRKTILTT  
 HC5 YIQITFVEPYFDEYEMKDRV TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRN TVLTT

FIG. 5A (cont.)

Coiled-Coil

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV  
IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV  
IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV  
SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSTDVDMIQLQLKLQGWV  
SHLFPYVKKRIPQVISQSSTEINPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV  
SHAFPYIKTRVNVTKEEIIITPIEVAIEDMQKKTQELAFATHQDPADPKMLQMLQVLQGSV  
MHAFPYIKTRISVIQKEEFVITPIEVAIEDMKKTLQLAVAINQEPPDAKMLQMLQVLQGSV

Coiled-Coil 2

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE  
SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE  
GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDAIRKNKSLIGPVQKE  
GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

Coiled-Coil 2

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS  
YQEEMKANYREMAKELSEIMHEQLG-----  
YQEEMKANYREIRKELSDIIIVPRICPGEDKRATKFP AHLQRHQRTDNKHSGSRVDQFILS  
YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAI SGTS DRGYGS PRYA  
YQEELRSHYKDMSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKA TPALPTVSISS  
YQRELG---KLSS-----PZ-----  
YQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

PBM

SSVVZ-----

CVTLPHPHVGTCFVMCKLRTTFRANHWF CQAQEEAMNGNGREKEPWTVI FNSRFYRSWGK

EVZ-----

SAEVZ-----

-----

-----

VHIFF

-----

-----

-----

-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

FIG. 5A (cont.)

	A	B	C
CLASP-1	YRVAFYGQ	YRVAFYGQ	
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEP	FRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEP	
CLASP-2		FEDEDGKEYIYKEP	
CLASP-6	FRVAFFGQ	FRVAFFGQ	FEDEDGKEYIYKEP
CLASP-4	FRVAFYGQ	FRVAFYGQ	SFFEEEDGKEYIYKEP
DOCK180	FAVGYYGQ	FAVGYYGQ	GFPTFLRGKVFIYRGKEYERRED
DOCK2	FAVGYYGQ	FAVGYYGQ	GFPSFLRNKVFIYRGKEYERRED
DOCK3	FRVGFYGR	FRVGFYGR	KFPFFLRNKEYVCRGH
KIAA0716	FRVGFYGK	FRVGFYGK	KFPFFLRNKEFVCRGH
CLASP-3	FRVGFYGT	FRVGFYGT	KFGDLDEQEFVYKEP
CONSENSUS	F V FYG YF	KEY K Q F R	
TRG	PKLTPLSEISQRLLKLYSDKFGSENVKMIODSGKVNPKDLSKFA	YIQVTHVTPFFDEKE	
CLASP-1	PKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYAY	IQVTVTPFFEEKE	
CLASP-2	PKLTPLSEISQRLLKLYSDKFGSENVKMTQDSGVNPKDLSKYAY	IQVTHVIPFFDEKE	
CLASP-4	PKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA	HIQVTVVKPYFDDKE	
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAY	IQITYVEPYFDTYE	
KIAA0716	HDYERLEAFQQRMLNEFPHAIA	MQHANQPDETIFQAEAQYLQIYAVTPIPESQE	
DOCK3	HDYERLEAFQQRMLSEFPQAVA	MQHPNHPDDAILQCDAQYLQIYAVTPIPDYD	
DOCK2	FQMQLMTQFPNAEK	MNTTSAPGDDVKNAPGQYIQCFTVQPVLDEHP	
DOCK180	EYERREDFQMQLMTQFPNAEK	MNTTSAPGDDVKNAPGQYIQCFTVQPVLDEHP	
CONSENSUS	L L Y M F	YIQ+ V P D L E	
	D	E	
CLASP-1	RTIITTSASHIFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN		
TRG	RTIITAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH		
KIAA1058	RTIITAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-2	RTIITAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-6	RTIITAIHCFPYVKKRIPFMYQHHTDLNPIEV: HDEMSSKKVAELR		
CLASP-4	RTIITTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELQ		
CLASP-3	KTIIITTSASHAFPYIKTRVNTHKEEIIILPIEVAIEDMQKKTQELA		
CLASP-5	NTVLTTCMHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLA		
KIAA0716	RTSILYLVQSLPGISRWFEEVKEVMSPLENAIEVLENKNQQLK		
DOCK2	RTSFVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL		
DOCK3	RTTITLTHSLPGISRWFEEVERRELVEVSPLENAIQVVENKNQELR		
DOCK180	RTSFVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL		
CONSENSUS	RT L F P V + V + P+E AI+ M + L F L L	I	

FIG. 5B

# CLASP/DOCK MOTIF

	F	G
CLASP-1	<u>SLOLKLOGSVSVKVNAGPMAYARAFLEETNAKKYPDNQV</u> - - K	<u>LKEIFRQFADACGQALD</u>
TRG	<u>KLOLKLOGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKV</u> - - K	<u>LKEVFRQFVEACGQALA</u>
KIAA1058	<u>KLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKV</u> - - K	<u>LKEVFRQFVEACGQALA</u>
CLASP-2	<u>KLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKV</u> - - K	<u>LKEVFRQFVEACGQALA</u>
CLASP-6	<u>KLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKV</u> - - K	<u>LKEVFRQFVEACGQALA</u>
CLASP-3	<u>MLQMVLQGSVGTVNQGPLEVAQVFLSE</u> - - I	<u>PSDPKLFRHHNKLRLCFKDFTKRCEDALR</u>
CLASP-4	<u>QLQLKLQGCVSVQVNAGPLAYARAFLND</u>	<u>SQASKYPPKKVSELKDMFRKFI</u> - - QACSIALE
CLASP-5	<u>MLQMVLQGSVGTVNQGPLEVAQVFLAE</u> - - I	<u>IPADPKLYRHHNKLRLCFKEFIMRCGEAVE</u>
KIAA0716	<u>PLTMCLNGVIDAAVNGGVSR</u> Y QEAFFVKEYILSHPEDGEKIAIRLRELMLEQAQILEFGLA	
DOCK2	<u>PLSMLLNGIVDPAVMGGFAK</u> Y EKAFFTEEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK	
DOCK3	<u>LLSMCLNGVIDAAVNGGIARY</u> QEAFFDKDYINKHPGDAEKITQLKELMQEQVHVLGVGLA	
DOCK180	<u>PLSMLLNGIVDPAVMGGFAK</u> Y EKAFFTEEYVRDHPAEAHEKIEKLKDLIAWQIPFLAEGIR	
CONSENSUS	L M L+G V VN G L I	Y AFL + V V F + P L+ I

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

FIG. 5B (cont.)

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr  
ref 1.1, 1.2 and 1.3

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 4A

722 752  
 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
 thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser  
  
 782 812  
 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
 trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys  
  
 842 Cadherin Cleavage 872  
 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
 val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val  
  
 902 932  
 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
 val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys  
  
 962 992  
 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
 asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly  
 ref 2.1  
  
 1022 1052  
 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
 phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr  
  
 1082 1112  
 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
 leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro  
  
 1142 1172  
 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
 leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu  
  
 1202 1232  
 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
 asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg  
  
 1262 1292  
 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
 glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu  
 ref 3.1  
  
 1322 1352  
 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
 lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala  
  
 1382 1412/471  
 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
 arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile  
  
 1442 1472  
 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
 asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser  
  
 1502 1532

FIG. 6A (cont.)

CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
 leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn  
 ref 4.1 and 4.2

1562 1592  
 AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
 ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652  
 ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
 thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp  
 ref 5.1 and 5.2

1682 1712  
 TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
 ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772  
 CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
 gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832  
 AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
 lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892  
 ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
 thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val  
 ref 6.1

1922 1952  
 TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
 cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 2012  
 GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
 gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072  
 ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
 met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132  
 AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
 ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

ref 7.1

2162 2192  
 ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
 thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222 2252  
 CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
 gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282 2312

FIG. 6A (cont.)

TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552  
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
GGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 Ixxxxxxxxxxxxxx Predicted  
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxx!  
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GGC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu  
ref 8.1

3002 3032  
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092  
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT  
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

ref 9.1

3122 3152  
 ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT  
 ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212  
 ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
 ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu  
 ref 10.1

3242 3272  
 TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC  
 tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332  
 CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
 pr lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392  
 GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC  
 asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452  
 TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
 phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln  
 ref 11.1

3482 3512  
 TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC  
 cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys arg ile

3542 3572 Ixxxxxxxxx Coiled-coil 1 xxxxxxx  
 CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG  
 pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602xxxxxxxxx Coiled coil 1 cont'd xxxx 3632xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA  
 ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys  
 ref 12.1

3662xxxxxxxxxxxxx ! 3692  
 CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT  
 leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752  
 GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG  
 ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812 Ixxxxxxxxxxxxxxxxxxxx  
 CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA  
 leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842xxxxxxxx Coiled coil 2 xxxxxxxx 3872xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA  
 arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3932 xxx

FIG. 6A (cont.)

ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
 met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr  
 3962 3992  
 AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
 ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr  
 4022 Ixxxx PBM xxxx|  
 ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
 met val his gly met thr ser ser ser val val STP  
 4082 4112  
 TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG  
 4142 4172  
 ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT  
 4202 4232  
 TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG  
 4262 4292  
 GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA  
 4322 4352  
 CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG  
 4382 4412  
 GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG  
 4442 ref 13.1 4472  
 CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA  
 4502 4532  
 GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA  
 4562 4592  
 TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT  
 4622 4652 ref 14.1  
 GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC  
 4682 4712  
 TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA  
 4742 4772  
 ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC  
 4802  
 TTT ACT

FIG. 6A (cont.)

## BAC sequences of Human CLASP 2

### Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTCAACAAAATTAGCAGTTGCTGCTCTG  
TGACAAAGTTGCACCATTGCAAGAAGAAAAAAATCCTAATGTGTTATATTACTATA  
TTTTACTCTATAGATCTTTCTAAAGAAAGAAAGTACAACGTAAAGTGTCTATATGTA  
TTCATATAAAATGACTAGTACAAGCATCATTGCAACAGATTCCCTTCATTGGAGG  
ATCTTCTTGTATTTGATGTTACACGATCAATTAGTCTTAATAAGATGAGGCTGGGTG  
TGGTGGCTCACACCTGTAATCCTAGCATTGGAGGCCAAGGTGGCAGATCACTTAG  
CCCAGGGGTTGAGACCAGCCTGGCCAACATGGCAAAACCTGCTCTACAAAAATAC  
NAAAATTATCCAGGCATGGTATGTGTCCTGAGTCCCAACTNCCTAGGAGGCTAGG  
GGTAGGGGGATTGCAAGAGGCTGGAGGGTCAAAGCCCNAANTGAGCCATTGGTNC  
ATGTCACTTGGACCCCAAGCNNGGGNGANCAAGAGCAAAGGACTNNTGTNNTTAN  
AAAAAAAACCGGGCTACCATACNNACCAACCCNNACCTACCCNACCTTCCANNTT  
AAAANAAGGCTTGNCTTGCANAGGAAAANAAAATNNCC

### Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTCTACAGTGTATACTNAGGTATGTGCTCCTNAACAAAATTAGCAGTTGCTG  
CTCTGTGACAAAGTTGCACCATTGCAAGAAGAAAAAAATCCTAATGTGTTATATTA  
CTATATTACTCTATAGATCTTTCTAAAGAAAGAAAGTACAACGTAAAGTGTCTTAT  
ATGTATTCATATAAAATGACTAGTACAAGCATCATTGCAACAGATTCCCTTCATT  
GGAGGATCTTGTATGTATTGACACGATCAATTAGTCTTAATAAGATGAGGC  
TGGGTGTGGCTCACACCTGTAATCCTAGCATTGGAGGCCAAGGTGGCAGATC  
ACTTAGCCCAGGGTTGAGACCAGCCTGGCCAACATGGCAAAACCTGCTCTACA  
AAAATACAAAAATTATCCAGGCATGGTATGTGTCCTGAGTCCAGCTACCTAGGA  
GGCTAGGGTAGGGGGATTGCAAGAGGCTNGGAGGTCAAGGCCCGAGTGAGCCATGG  
TCATGTCACTGCACCCCCAGCCAGGGCCGACAGGAGCAAGACTNTGTNTCAAAAAAA  
AACAGNAACCAACANCCAACAACAACNACCTTCNGCAAAANAAGCTTGCTNCA  
ANGAAAACCAAAATGNCTTCTTNTTCCCCCN

### Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCNCTACNCCACTTTAACCTTTGAAAACACAGTGTTCNCTCAANTATGC  
GCTCCTCACATATTAGCAGTTGCTGCTGTGACATAGTGCACCAATTNTGCAAGAAG  
AAAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTNTCTAAAGAAAG  
AAAGTCAACTGATGTGCTTATATGTATNCATATAAAATGACTAGTACATGCATCATTG  
CAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTGACACGATNANTATTA  
GTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGANGCATGT

Fig. 6A (cont.)

GGCAGACACTTANCCNCGGTNGAGACAGACTGTCACTGNCAACTGTCTCTNTAAANCA  
AANNCTCCGCNGGNGATGGGCTGAGCCAGTCCTAGNNNGCTAGNTAGNGATGNNNGAGN  
TGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCACACGNTCTGT  
TCNAAAACATACCAACACACACTNCACCTNCGAAAATTGCTCTNNAAANATGCTTNT  
TTCACACNGNTNCAATCNCTATATNNNTCTTCTATTCTNCACGTNTNATTANNATCTT  
CNCTGCANAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTACGCTTATAGCTC  
CCCTACACNTNNCAGCNNTNCNNGTGAAGGGCCNCCGAATCTACGANCATACTCTC  
TCCGTATATNGCCTCGGTANCGCCATCTGCTNTNCTCNCTNGCNNTNANCNG  
TNCGCTATCTCTNNNCCGGATCCNCNCCATATNNNTNCTACTTANAGCGTAANNTNT  
NCNCNCACTANTCACAACTTNTNCNTNNAACTCTATCTNCTCCTCTTACCCACCTCACT  
TACTACCTNTTCACNCANTCTCCTCNCTNTCCACTGATCTCCACATAGCTGCTNTACTC  
GCCANTTTATCATATNCACACNCTTACGCTNNNTNT

**Ref 2.1**

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGTATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGAT  
ATTTTATACAGGATTCTAAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTAGC  
TTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTCAGGATGGCTGC  
AGGGATTGATTGAAAACTAAGGACACATTCAATAAAACAATGTCTTCAATTGATTTTT  
AGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACAGGCTC  
AAATACAATAAAAAAATTAGTAAGGCAGAGCTTAAAAAAAAAAAGGAAAAAGATAAA  
TTCTTACAGAGAAAGGCTACATGGTGACTTCTGTTACCAAGTAACAACCCCCGCACTACC  
TTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAGACAAAGC  
CCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAACAAGCAAAAAAGTTATTCA  
GGTCCAAACATTCCGAAATTGGATTCAAAGCAGGCATTATTGCTAATAAGTTATC  
CACTGACATAAAAACATGCCCTCAACATTGCCAGAGCACCTACTCTATTNTAGTCNCN

**Ref 3.1**

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACAAACAGAGGCAGGTAGAGGGTGGCTATCCTGCCTGATGGCTCTGA  
AAAGAAGACACACATGGTAAGTTGACCCAGGATTCTGAGAACCGAACTAAGTTGGTG  
CTGACCATCTCCTTATTGGATCCTCCTATAAAAGACAGATATTGATTAGTCCCAA  
AATAGAGCAAAATCTTAGTGTGTTACCATGAATTCTAACTGATTACTTCTTACAC  
CACTAAAATAAAGGACATTATCAATGCACATTCCCTCATTGGGGACCACTCACCTT  
GAAGCATATCTGTCAAAAGAATGCTTATCAGCAGGTTCTGAGCACACTGATGGC  
GATCAGACGGACCTCCCGAACCTCTGGAGGGCTGCCCCACCTCCCTNAGTAACAGT  
CCCACCAAGAAGTGGTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGCTGGGAGG  
TCTGAAATGAGGATAGAAACTACTTGNGTTAGGAAAGATGCAATGCTCTTTGAATA  
AAACAAACAAACAAACNAACAAAAAAACTAAGACCCATCCTNTGNATTCAA  
GCCCAACCTGGGTNGGTCAAAGAGATGATCAGNANTTGGCNTNAAATGAAGAAAG  
AAATNAATTNTCCAGGGNTGTTCTNCTTTAGCACANGGAGGGATNTTAANTGAAA  
ACCAATTAAATCCAATTNAGGNG

**Ref 4.1**

FIG. 6A (cont.)

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTCTGCAAGGCTGTTCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGCA  
TTTCTCACACTGTTGATGTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAATC  
AAGCCAACAATAAAAGTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACCTTA  
AGGGAAATTGCTTTATTGCACTTATTTCTGTTAGGAAGTTGGCTCAAGAGTTGCAT  
TCCATTACTTCACCTTAAAGAACCAAGGTCAATACAAATGAGATAAAAAGAAAAGTAGT  
CTGAAACATTCAAGATGTAACATCAATTCACTGTTAGAAACCACCTTGATCGCTAAA  
GACTAAATGCATAACCTGTTCAAGATGTGATAGAATGAAGACTTAAAAAAATTAAAAG  
ATAAAATCCACCTACAACATCAAATCACAAAATTAAACCACACAACAAACTTGTAGCA  
TTCAAACACTGGTAATAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCATGGGTA  
TTTAAATTTCGAGGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTGCTGTTNA  
GCAGCAGGTTGGTGCTATGCTCCTTTGAAGACATATTGTGAAGCTGGTATTTGG  
GGGCCTGCTTATGATAAAANGCAAGGTNTCAATGNAGGGGN

#### Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC  
ATTTCACACTGTTGATGTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAAT  
CAAGCCAACAATAAAAGTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACCTT  
AAGGGAAATTGCTTTATTGCACTTATTTCTGTTAGGAAGTTGGCTCAAGAGTTGC  
ATTCCATTACTTCACCTTAAAGAACCAAGGTCAATACAAATGAGATAAAAAGAAAAGTA  
GTCTGAAACATTCAAGATGTAACATCAATTCACTGTTAGAAACCACCTTGATCGCTA  
AAGACTAAATGCATAACCTGTTCAAGATGTGATAGAATGAAGACTTAAAAAAATTAAA  
AGATAAAATCCACCTACAACATCAAATCACAAAATTAAACCNCACAACAAACTTGTAG  
CATTCAAACACTGGTAATAAACACTGAGGAGCCTACCCAACTTGAGGGGTGTCATGG  
GGTNTTTAAATTTCGNGGGANANCCAGTGNATGGTGACCTCACCCAAAGAACGC  
TTGTTGTTNACCAAGCNAGGTTGNCTNTGCTCCTTTAGAANACNNNTTTNNNN  
AAATNCTGGNTTTTNNNGGGCCCCCTNCNTNNNT

#### Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCCTGGATAAGGTAATTGCTTTACCCAAACACAAATGTTCTTATAATCAATGGATT  
AGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTAAAGTGTGACCTTGTGTTTTT  
CTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTAAAGGTTGGGGCCCATT  
CTTGAAGTGCCTGATTCCCTGTTCCAGTACCTCAGATCCTGGCAGGGTTGCAGTGG  
AGCGTCTTGAGTGAATGGCTCTGGTGGGTGAACGGGGAGGGACTAAAATGCTGCC  
ATCTCAATTCCCTGAGTCTTTATTATTATTGAGACAGAGTCTCGCT  
GTCGCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCTCCGCCTCC:TG  
GGTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC:TGGGACCAACAGGCACAAGCC  
ACCACCGCCCCGCTAATTGTTGTNTTTAGTA:GAGAT:GGGGTTCAACCATTGGC  
CAGGCTGGCTAAACTCCTGACC:TCGTCACTCGCNCCTCGGNCTNCCAAAGTGCTT  
GGGATTNCAGGCNGTGAGCCCACTTACACCTNGGGCAATTCCCTGTNAGTCTTTTAC  
CAGAGACACCATCAACACAGCTTCCACCCACAA

FIG. 6A (cont.)

### Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTCCGGATAAGGTAATTGCTTTACCCAACACAAATGTTCTTAT  
AATCAATGGATTAGCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTAAGTGTGA  
CCTTTGTTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGG  
TTGGGGCCCATTCCCTGAAGTGCTCTGATTCCCTGTTCCAGTACCTCAGATCCTGGGCA  
GGGTTGCAGTGGAGCGTCTGAGTGAATGGCTCTGGTGGGTGAACGGGGAGGGACT  
CAAAATGCTGCCATCTCAATTCCGTAGTCTTTATTATTATTATTGAGAC  
AGAGTCTCGCTCTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAATTCACTGCAA  
CCTCCGNCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGCAGCCTGGGAA  
CCACAGGCTCANGCCACCACGCCGGCTAATTNTGTAATTNAGTAANAAAATTGGG  
GGTTCTCACCATTGGCCCAAGNCTGGGCCTAAAAACCTNCTNACCNTCGNCATT  
NCNCCCCNACCNTGGCNCTNCTCAAANGNGCTGGGATTANCANNGCNTAAC  
CCCCNTATCACCGTGGNCCTTAATT



### Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGTTNAGNCCTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGGG  
CTTCAGGTACTGGGTATCTGGAGCCTGCTGTTGCATTGCTAGTGCATCAGACCAAG  
GGCTTTCTCCCTGTAGCTGCTACTTATACACATAGCTCTAACAGATGATTCTCCA  
GACAACGTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCCTCTAGGAGTGTCTCCT  
TTCTTGAAAGAGATCATGAGGGCTAGATTGTAATGAAGTGAGGCTCAGTGCTTGA  
GCACATCCGGTAAAAGTCCAATATATTGGTCATAAAGTTCTCATTCTTATAGCAGT  
TAATTCTCTGGCTCATGAGTTCTTAGTTAATCTGACTTTAAATTAAATGTCTCCA  
GCACCAAGTCATATCCCCAGGGCAAACCTCAAAGGCATGAGAGGCCAGACTCGGGCCTG  
GTCATAGCAACCCCTGCTAGGGCCTGGTCCCTGCCTCCGCTTGTGTGCTGGCGCA  
GGCCTATGGGCCCTAGGAAACAGGACCACCCCTGTCGACCCCTACAGAGACCAGC  
CAAGTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCAGTTCTGCTAAAACA  
GGTTAACGCCTGCAGCCACTTATCTGTAACTGGCNGAGGTTTGACATAAAA

### Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTCTATTAACATTGGCGTTAAGGTGTATCAATTGCTGTTCG  
NGGTTCTAGTTACCTTCACATTCAATTCTGCTGGTAAGCTCAGTGAGCACAAACTTA  
CTATGTTGCATTTCAGCAATTATTTGTCCCTGTAAGGAAACCATTAAATCTTT  
AAATTCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATAAAATT  
AACTGGTCAGTGTGTGCTGCGCGCTGGTATGGTGGAAACACGGTCTCTGGAGGCAG  
TTAACTCTGGCTCGAACCTTGAGGGATGGTGAATATAGGCACCTAATCAGGCATTCTG  
CCTTGAATATCTTAAATATCCAAATGTTAGCGTTAATTAGATTATGTAGAA  
AGGAGCAATAAACACAAGACACATGTTTCAGTTTATCTGTTACTGCATTAAATGA

FIG. 6A (cont.)

TAAAAACGTTGGAGATAGAAAATGAAAGGGTTTTGTCTGTTAAAGTT  
TTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTCACCACTCTCCTGTTTAGG  
AACCCAATACTTTCTTGCATTGCTAAATGATTACTCCATTCTAGCATAGAAAAGGA  
AAAAATTGGAATGAGTGTATAT

**Ref 8.1**

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTNAATNCCAGCCGCTACTGCGGGCGNTNAATCGAAACGTGTTNTCTGT  
GATGCCTGGCTCTGATTGTGTGGATTGGTCATCAGTGGCGGTGGCAGNTGGGGTCA  
TGGAAAGCGGCCATGGGGACTGATGGCAGGCCCTGGATTGCCACCGCAGAGCCTGGCA  
GTGTCTTGGTCTGCATTCTACCGCGAAGTCTCATTCACCTCACGTGTTATCTCTTG  
GAAAGCATTCTTTAGCGGGCTGTGTCTACCCCTCCATCCTCTCGTCCAAACTCCCCCTC  
CTTCTCTGTTCTGTCTCCTCCCATTCTCTCCCCAGTTCTTCTCCTATGTTCTTCC  
CAGTGGTTCTTCCTCTGTTGACTTCCAAGGTCAATTGACTGTTCTGCTCCAA  
CTACAAAGATACTAAAATCTCACCTAACCAACTCTTCTTCTTAATGAAAGAATGTT  
TTCAGTCCATCCCAAATTGTGTGGACTTCACAAACCTCTAAATGGAGCCTTTCT  
CTTCCTACTCTGACTAGNTGGTAAACGCTCCATGTTCTGGCCAGAACTCCCTGGTGA  
GTAGCGTCACTCCACTTCTGTGCAGAACCAAGCCTCAGAAAAACTCCTTGCANC  
TGAGTGGGTTGGGACACGCCCTTNTTGGG

**Ref 9.1**

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNTATCCGNTCAGTTANAGGAGTCTCTGAGAAATTCCGACAGCGGT  
GTGAGTTGGGTTCTTGTAAATATACTCCTTCCATCTCATCTCAAAGAATCCCTGT  
GACATAAAGCACAAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACACACCTAGGA  
AGCGTTCTTATTACAAGGGGGAAAAAAAGGAATGGTCTAAAAATCCAGCTGAAAT  
GGGCTTCTGAATGAGAAAGAAAATGCTAATAACATGAAGTCTAGGTGCAAAGGTAAA  
GGAAAAACACAAACATTGCAAACCTATTCAAGAATGCAGTCATTAAAGTGTGAGTAAA  
TGAAAGATTGGATACAAGACTAAGCTGTCCCAGGGAAAGTCTAATGGGAGTCAAGCC  
TGTTCACTTCCAAGAACGAGAACACTCACTANAAAATGATGAGCAGCCCACGACAGG  
CAGGCTCAGAACGTGGACATGCCTCCCTCTGATGGCTNCCATGCACACAGGATT  
ATGGCATGAACTGAAGCGTTGGGGTCTGGAGTAAGTTAGTAAAAGTTAGGTAAAG  
CTTGTATAAAATTGTATTTGCTTACCCGATGAGAAAAAAATATTNAAGACCTGGTA  
GCTTCAATATTCAAGAAAAATATTTCATNTCACCCG

**Ref 10.1**

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACCTNCTTAAACTGTACTCGGATNA  
ATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTTG  
GANAAGTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTAAATG  
TNTATAGAAAAACACANGAAAAATATTAAGGATTGTTGGCCGTGAGTGGCAGGTG  
TATNTTCTNCTGATCCTTAGNGCTTCCATTACATGCNTGACATTAAAAANCTTTA

FIG. 6A (cont.)

TCGCCTAATTTGAAACATCTAATTTACAAAATAATTACCGTNTGCCANGNATAT  
TNTCATTAGGNCCAGCTATTAGAAACTCTGACANAAATGAGGGGCTGTGGCTTNC  
CTNCCTNNACTGNCCCTCTTCNNGNATGTACCACATGAACCTGNCNCCTCTTCNNC  
TNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNGGCNGGANTNGGTN  
NAATTGGGACACAATGGTACNANGCTATNGGAATNGAAACTCTCCNACNNNCNGT  
GNCCNTGGGAAAATGNGCNNATTCAATTN

**Ref 11.1**

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTNNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGCACGAGCCNGGA  
CACGCTCGGCAAAGAGCTGTCCAGAGGGATTCAAAGCTTCAGGACTGGAAGGGTCTT  
TCGAGCTCAGTTAGCCACCCCCACACCCATTTCAGTTCACATTATCTAGTGCTTCCTT  
TTGAATACTTGGGATGTTTCTGTTGATCTGTTGGCACTTCCTTCCACAAGACCAAG  
AAGCTCATATCCAATCTAAGGTCACTTACCCCTCTGAGAATCTGATGAAAATGGCGTGC  
CTTATGTGCCTAGATGCTTTGCACACAGTCTAAGGTGACTTATGGACTCCAGGTCCAG  
CAGCCACACCCAGTCCTGGTCTCCGCACAGGGAGGGACCCGTCTCACACACCTGTCT  
CAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAAATGGGATGTGAG  
CTTGGATCGCCCCACGCTGTTGNCACGGGGCTTGGCCAGCTGGCCACTNGAAAT  
GCCTCCTTGTCCCAGGAAAGCTCACTGCATTCAATGGGNTNTCCACGAAGTTCAN  
CTTANGGG

**Ref 12.1**

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAAGGTGAGCCAGGCACAGCAGGC  
CGGAGGGCAGCAGGGACGTCCCTGCCCTGGGTGACTTGAGAGTCGTTCCACTAAC  
AAGGTCTACTTGAGAGCCTCGGTTACCAAGTGATCCCTGCTCCCTCCCCAACGTNT  
GTGACATTCTCCTGATATCAGAGGGGAGGAAACCTCATGATCCCTGCCCTGGCC  
ATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTGTCAG  
TATTGGGAATTCTGGGTGCCTGATTAGAACATCAAGACTCTTCTAAATNCAAAGA  
AGTGTGGAGAGCAGTAGATTTCCTATAAAACTGGTGTGCTGGTTCTATGAAAATTG  
GATCCAAAAAAAGTCCTTAAGTTACCCTCTTAATGGNATCTTTGATTATGGAATT  
ATTATTAAATAGCCAATCAATCCAATTTCCTTATTGGTAGCATTTATGTTCTC  
TTTAAAAAAATCTGGNCTACCTCCAAAATTCAACAGATGTTCTCTAGGGTTTCCTCC  
TTTGGTTCAAGCATCCCATTCAANGTCTGCAGTCCATTCTGGGG

**Ref 13.1**

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTATTCTCCTTGCAGAGTAGTGTAGAATAGATGGCCTACAGAAAAAAA  
AGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGACCT  
TTTGCCTCGAGGCTGAGCTGGAAAATCTGAAAATATTTCCTGTGGCACATT  
AGGTTGAATACAAGAACTATTGTGACTATGTTGATGACCTAACAGGAACGTGACC  
ATTGTAATTGTGACTGACCTAACAGAGATTAAAGTGTCTTATATTCAATTCTGC

FIG. 6A (cont.)

ATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAAGTCAAGCANTT  
TAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTAAAAAGNACAAAGTAGTACA  
GNATATTGNTATGTACATATCATTGGTAATACACACNCCNGGCNTCTGTACATATATGT  
ATTACATTCTACNTTTAATAACTCCCNTGGGCTTATGCCNTTAAGGTTAANTTNGAT  
AAATTNGGCTGTTCCNGTNTATNCNATACNCTTT

### Ref 14.1

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA  
CATAAACAATATACTGTACTACTTGTACTTTCAAGCATAGTTGCCGGTTATTAATATAGG  
CCTTTGGTTCTAAACTGCTTGACTAGTTAAGCTCACATAATTCCCTTAAGCTTCATAT  
TTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCACTGGTACAA  
AAATTACAATGGTCAGTTCCCTTAGGTCAATCAAAAAACTAGTCACAAAAAATAGTTCTTGT  
ATTCAACCTGAATGTGCCACAGGAAAAAAATATTTCAGGATTTCCAGCTCAGC  
CTCGAGGCAAAAGGCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGTAGATC  
CCAGAACCTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAGAATAAA  
ATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTGTAAAGACACAATGAAAAACTT  
GGATATTGGCAGGNGAGATTTAAAAAAATGTGCCCTTCTTACCACTCCTATAGNA  
AAGTCTGGTTAAGAAATAACCGTTGGTCTTATTTCCTTTNTTCCCCCTCCCTGGG  
NCTTCCTGGGGCTCGG

FIG. 6A (cont.)

HC2A	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
KIAA	-----
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPIFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFRSAFAAVLHHHQNPIFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHL <del>LL</del> FFHVSCDNSSKGSTKKR <del>V</del> VETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHL <del>LL</del> FFHVSCDNSSKGSTKKR <del>V</del> VETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI <del>A</del> FLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI <del>A</del> FLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCP <del>M</del> V
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTVTRV
HC3	-----NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSN <del>S</del> WVNTGGPKAAPWGSNPSPSAES
HC5	-----

Fig. 6B (cont.)

HC2A IIHVVAQCHE ESHLRSYV KYAYKAEPYVASEYKTVHEELI MTTILKPSADFLTSN  
 KIAA IIHVVAQCHE ESHLRSYV KYAYKAEPYVASEYKTVHEELI MTTILKPSADFLTSN  
 rat -----  
 HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN  
 HC1 LPDIVAKCHEEQLDHQS VQSYIKFVFKTR--ACKERPVHEDLAKNVTGLLK-SNDSPTVK  
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKL FHEELALQWVVCVG--SVR---E  
 HC5 -----

Cadherin  
Cleavage

HC2A KLLRYSWFFF DVL IKSMAQH LIEN SKV KLI RNQRFP ASYHAA ETVV NMLMPH ITQK FGD 2.1  
 KIAA KLLKYSWFFF DVL IKSMAQH LIEN SKV KLI RNQRFP ASYHAA ETVV NMLMPH ITQK FGD 1.1 / 2.1  
 rat -----  
 HC4 KLLKYSWFFF EIIAKSMATYLLEENKIKLTHGQRFPKAYH HALHSLFLAIT-IVESQYAE 6.1  
 HC1 HVLKHSWFFF AIILKSMAQH LIDTNKIQLERPQRFPESYQNE LDNL VMLSDHVIW KYKD 1.1 / 2.1  
 HC3 SALQQAWFFF ELMV KSMV HHL YFNDKLEA PRKSRF PER FMDDIA ALV STIAS DIV SRF QK 1.1 / 2.1  
 HC5 -----

HC2A NPEASKNAHSLAVFIKRCFTFMDRGFVKQIN---NYIS--CFAPGDPKTLFEYKFEFL 2.1  
 KIAA NPEASKNAHSLAVFIKRCFTFMDRGFVKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 rat -----  
 HC4 IPKESRNVN YSLASFLKCCLTLMDRGFVN LIN---DYIS--GFSPKDPKV LAEYKFEFL 7.1  
 HC1 ALEETRRATHS VARFLKRCFTFMDRGCVFKMV N---NYIS--MFSSGDLKTL CQYKFDL 3.1 / 3.2  
 HC3 DTEMVERLNTSLAFFLNDLLSVM DRGFVFS LIKSCYKQVSSKLYSLPNPSV IYSLR LDFL 3.1 / 3.2  
 HC5 -----

HC2A RVVCNHEHYIPLNLP M-----PFGKGRIQR-----YQDLQL-----DYSLTDEF 4.1 / 4.2  
 KIAA RVVCNHEHYIPLNLP M-----PFGKGRIQR-----YQDLQL-----DYSLTDEF  
 rat -----  
 HC4 QTICNHEHYIPLNLP M-----AFAKPKLQR-----VQDSNL-----EYSL SDEY  
 HC1 QEVCQHEHFIPLCLPIRSANIPDPLTPSES-----TQELHASDMPEY SVTNEF  
 HC3 RIICSH EHYVTLNLP CSLLTPPAS PPSVSSAT SQSSGF STNVQDQKIANMFELS--VPF 4.1 / 4.2  
 HC5 -----MNADTAP TSPCPSIS---SQN SSSCSSF QDQKIA SMFDRTS RVP A

HC2A CRNHFLVGLLL REVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT 3.1  
 KIAA CRNHFLVGLLL REVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGLLL RETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ 8.1  
 HC1 CRKHFLIGILL REVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQ A QIAS  
 HC3 RQQHYLAGLVLTEL A VILD PDAEGL FGLHKKV INMVHNLLSSHDSDPRYSDPQIKARVAM  
 HC5 SSTS-SPG LLFTEL A A LDAE GEGE GISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAA

HC2A LYLPLFGLLI ENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH 9.1  
 KIAA LYLPLFGLLI ENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 rat -----  
 HC4 LYL PFVG LLL ENIQR LAGRD TLYSCAAMPNSASRDEFPCG---FTSP--AN--RG SLS  
 HC1 LYMP LYGM LLDNMP RIYLKDLYPFTVNTSNGSR DDLSTNGGFQSQTAIKHAN SVDT SFS  
 HC3 LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE-----SG---SMIS  
 HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

4.1 / 4.2

HC2A KDLLGAI SGIA SPYTTSTPNIN SVRNAD SRGSLI STD GNSL PERN SEKNSL DKHQ QSS 5.1 / 5.2  
 KIAA KDLLGAI SGIA SPYTTSTPNIN SVRNAD SRGSLI STD GNSL PERN SEKNSL DKHQ QSS  
 rat -----  
 HC4 TDKDTAYGSFQNG-----HGIKRED SRGSLIP-EGATGFPDQGNTGEN-----TRQ S 10.1  
 HC1 KDV LNSIA AFSS-----IAI STVN HAD SRAS LASL DSNP STNEK S SEK TDNCE KIPRPL  
 HC3 QTVAMAIAGT SVPQ-----LTRPGSFLLTSTSGRQHT----- 3.1  
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN----- 2.1

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSSDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSSDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSII DVCL
HC3	-----TFSAEASSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

11.1 / 11.2

HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----	QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----	TGMM
rat	-----	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----	QTMPALRNRSGVM
HC1	QNFRYLGKRNIIRKIAAAF--KVFQSTQNNGTLKGSNPSCQTSGLLAQWMHSTS RHEGHK	
HC3	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----	LEEAIILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KS RDVKAR-----	LEEALLRGE GARGE MM

6-1

HC2A	HARLQQL-----GSLDNS-----LTFNHSGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADI FHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMT SNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDOEALISGNLATEAH

12.1 / 12.2  
6.1 / 6.2

HC2A	LTALDTLSLFTLAFK <b>N</b> QLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFK <b>N</b> QLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3	LIILDLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAYLQHCFATORALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRLIA

7.1

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCCTS KISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	<del>KFPELLFEEETEQCADLCLRLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK</del>
HC5	KFGDLLFEEEVEQCFDLCHQVLHHCSSMDVTRSOACATLYLLMRFSFGATS--NFARVK

13.1

HC2A	LQVIISVSQLIADVVGIGETRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGGTRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGGTRFQQQLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3	MQVPMSSLSSLVGTSQNNEEFLRRSLKTIILTYAEEDLELRETTFPDQVQDLVFNLHMLS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMOMTPFPTOVEELLCNLNSILY

14.1/14.2/15.1/15.

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTLDMSMARIHVKNGLSEAAMCYVHV  
ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTLDMSMARIHVKNGLSEAAMCYVHV  
ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTLDMSMARIHVKNGLSEAAMCYVHV  
ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTLDMSMAKIHVKNGLSEAAMCYVHV  
ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI  
DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMGKHSERSNHAEEAQCLVHS  
DTVKMREFQEDPEMLIDLMYRIAKSYQASPDRLRTWLQNMAEKHTKKCYTEAMCLVHA

16.1 / 16.2

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

		SH3	
TALVAEYI	TRKGV		-FROGCTAFRVITPN
TALVAEYI	TRKEA		-VQWEPPILLPHSHSACLRRSRGGVFRQGCTAFRVITPN
TALVAEYI	TRKEAD		-LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
AALVAEFL	HRKKL		-FPNGCSAFKKITPN
AALIAEYI	KRKGYWKVEKICTASLLSEDTHPCDSNSLLTPSGGSMFSMGWPAFLSITPN		
AALVAEYI	SMLED		-RKYLPVGCVTFO <del>N</del> ISSN
AALVAEYI	SMLED		-HSYLPVGSVS <del>F</del> QNISSN

9.1 / 8.2

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

I DEEAASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  
I DEEAASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  
I DEEAASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERLRAGLTSINSSSP  
I DEEGAMKEDAGMMD-----VHYSEEVILLEQCVNGLWKAERYEIISEISKLIGPI  
I KEEGAAKEDSGMHD-----TPYNE~~N~~ILVEQLYMCGEFLWKSERYELIADVNKPIIAV  
VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASF~~SMAGMY~~EA~~V~~NEVYKVL~~Y~~PI  
VLEESVVSEDTLSPDEDGV~~C~~AGQYFTESGLVGLLEQAAELF~~ST~~GG~~Y~~ETV~~NE~~VYK~~V~~LI~~Y~~PI

9.1

17.1 / 17.2

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

ITAM	ITAM	ITAM	ITAM
YEKRD			
YEKRD <del>FERLAHLY</del> DTL <del>HRA</del> YSKV <del>TEVMHSGRLLGT</del> <del>F</del> RV <del>A</del> FFGQAAQYQFTDSETDVE			
SMKSGGT <del>LETTHLY</del> DTL <del>HRE</del> YSKV <del>TEV</del> ITR			-A---AGSWD <del>LLPGGLFGQ</del>
YENREFENLTQVYRTL <del>HGAYTKI</del> LEV <del>MHTKKRLLG</del>			-TE <del>ERVAFYGQ</del>
FEKQRDFKKLSDIY <del>YD</del> I <del>HRS</del> Y <del>LKVAEVVN</del> SEKRLFG			-R <del>YRVAFYGQ</del>
HEANRDAKKLSTI <del>HGKL</del> Q <del>EAF</del> FSKIV <del>HQ</del> STGWERMFG			-TY <del>FRVGFY</del> G-
LEAHREFRKLT <del>LTHSKL</del> Q <del>RAF</del> DSI <del>V</del> NKD <del>H</del> --KRMFG			-TY <del>FRVGF</del> FG-

9.1

9.1

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

-FFEDEDGKEYIYKEPKL~~TP~~SEISQRLLKLYSDKFGSENV~~KM~~IQDSGK~~V~~NP~~K~~D~~L~~DSKYA  
GFFEDEDGKEYIYKEPKL~~TP~~SEISQRLLKLYSDKFGSENV~~KM~~IQDSGK~~V~~NP~~K~~D~~L~~DSKYA  
GFFEDEDGKEYIYKEPKL~~TP~~SEISQRLLKLYSDKFGSENV~~KM~~IQDSGK~~V~~NP~~K~~D~~L~~DSKFA  
SFEEEDGKEYIYKEPKL~~TG~~LSEISLRLV~~KLY~~GEKFGTENV~~KI~~IQDS~~D~~KVNAKELDPKYA  
GFFEEE~~E~~EDGKEYIYKEPKL~~TG~~LSEISQRLLKLYADKFGADNV~~KI~~IQDS~~N~~KVNP~~K~~D~~L~~DPKYA  
TKEGBLDEQEFVYKEPAITKLA~~E~~ISHR~~I~~E~~G~~FY~~G~~ER~~F~~GEDV~~V~~EV~~I~~KDS~~N~~P~~V~~D~~K~~C~~K~~L~~D~~PNKA  
SKFGDLDEQEFVYKEPAITKL~~P~~EISHR~~L~~AFY~~G~~Q~~C~~FGAE~~F~~VE~~V~~I~~K~~D~~S~~T~~P~~V~~D~~K~~T~~L~~D~~PNKA

10.1

10.1 / 10.2  
4.1

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

YIQVTHV~~I~~PF~~F~~DE~~K~~E~~L~~Q~~E~~R~~K~~T~~E~~F~~E~~R~~S~~H~~N~~I~~RR~~F~~F~~EMP~~F~~T~~Q~~T~~G~~K~~R~~Q~~G~~G~~V~~E~~E~~Q~~C~~K~~R~~R~~T~~IL~~T~~A  
YIQVTHV~~I~~PF~~F~~DE~~K~~E~~L~~Q~~E~~R~~K~~T~~E~~F~~E~~R~~S~~H~~N~~I~~RR~~F~~F~~EMP~~F~~T~~Q~~T~~G~~K~~R~~Q~~G~~G~~V~~E~~E~~Q~~C~~K~~R~~R~~T~~IL~~T~~A  
YIQVTHV~~T~~PF~~F~~DE~~K~~E~~L~~Q~~E~~R~~K~~T~~E~~F~~E~~R~~S~~H~~N~~I~~RR~~F~~F~~EMP~~F~~T~~Q~~T~~G~~K~~R~~Q~~G~~G~~V~~E~~E~~Q~~C~~K~~R~~R~~T~~IL~~T~~A  
HIQVTV~~V~~K~~P~~Y~~F~~DD~~K~~E~~L~~TER~~K~~T~~E~~F~~E~~R~~S~~H~~N~~I~~SR~~V~~F~~A~~P~~Y~~T~~LS~~G~~KK~~Q~~G~~C~~I~~E~~Q~~C~~K~~R~~R~~T~~IL~~T~~T  
YIQVTV~~V~~T~~P~~F~~F~~E~~E~~E~~K~~I~~E~~DR~~K~~T~~D~~F~~E~~M~~H~~H~~N~~I~~N~~R~~F~~V~~F~~E~~T~~P~~F~~TL~~S~~G~~K~~KK~~H~~GG~~V~~A~~E~~Q~~C~~K~~R~~R~~T~~IL~~T~~T  
YIQITV~~V~~E~~P~~Y~~F~~D~~T~~Y~~E~~M~~K~~D~~R~~I~~T~~Y~~F~~D~~K~~N~~Y~~N~~L~~RR~~F~~MY~~C~~T~~P~~FT~~L~~D~~G~~R~~A~~G~~E~~L~~H~~E~~Q~~F~~K~~R~~K~~T~~I~~L~~T~~T  
YIQITV~~V~~E~~P~~Y~~F~~D~~E~~Y~~E~~M~~K~~D~~R~~V~~T~~Y~~F~~E~~K~~N~~F~~N~~L~~RR~~F~~MY~~T~~T~~P~~FT~~L~~E~~G~~R~~P~~R~~G~~E~~L~~H~~E~~Q~~Y~~R~~R~~N~~T~~V~~L~~T

10.1

4.1

11.1 / 11.2

18.1

Coiled-Coil

HC2A IHCFPYVKKRIPVQHHTDLNIEVAIDEMSKVVAELRQLCSSAEVDMIKLQLKLQGSV  
 KIAA IHCFPYVKKRIPVQHHTDLNIEVAIDEMSKVVAELRQLCSSAEVDMIKLQLKLQGSV  
 rat IHCFPYVKKRIPVQHHTDLNIEVAIDEMSKVVAELHQLCSSAEVDMIKLQLKLQGSV  
 HC4 SNSFPYVKKRIPINCEQQINLKEDGATDEIKDKTAELQKLCSTDVDMIQLQLKLQGSV  
 HC1 SHLFPYVKKRIPQVISQSSTELNIEVAIDEMSRKVSelnQLCTMEEVDMISLQLKLQGSV  
 HC3 SHAFPYIKTRVNVTKEEILTHEVAIEDMQKKTQELAFATHQDPADPKMLQMVQLQGSV  
 HC5 MHAFPYIKTRISVIQKEEFVLTHEVAIEDMKKKTQLAVAINQEPPDAKMLQMVQLQGSV

11.1

Coiled-Coil 2

HC2A SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
 KIAA SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
 rat SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  
 HC4 SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE  
 HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE  
 HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE  
 HC5 GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

11.1 / 12.1

Coiled-Coil 2

HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHI FNAISGTPSTMVHGMTSS  
 KIAA YQEEMKANYREMAKELSEIMHEQLG-----  
 rat YQEEMKANYREIRKELSDIIIVPRICPGEDKRATKFP AHLQRHQRDTNKHSGSRVDQFILS  
 HC4 YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA  
 HC1 YQEELRSHYKDMSELSTVMNEQITGRDDLSK---RGVDQTCTRISKATPALPTVSISS  
 HC3 YQRELG---KLSS---PZ-----  
 HC5 YQQELKKNNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

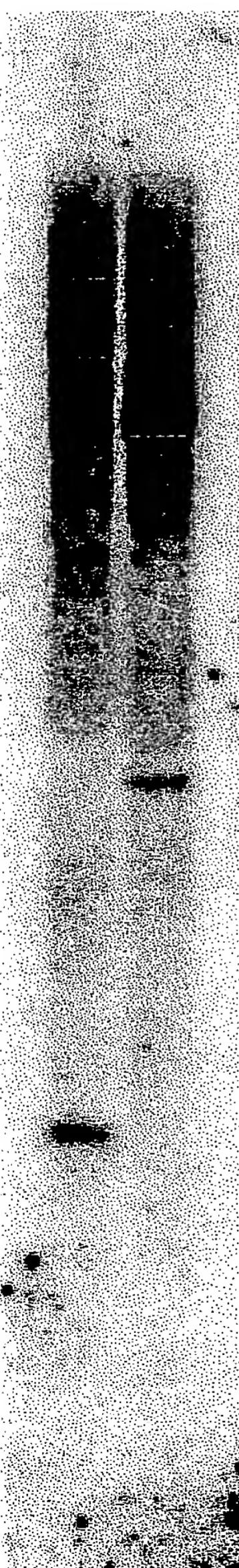
19.1

PBM

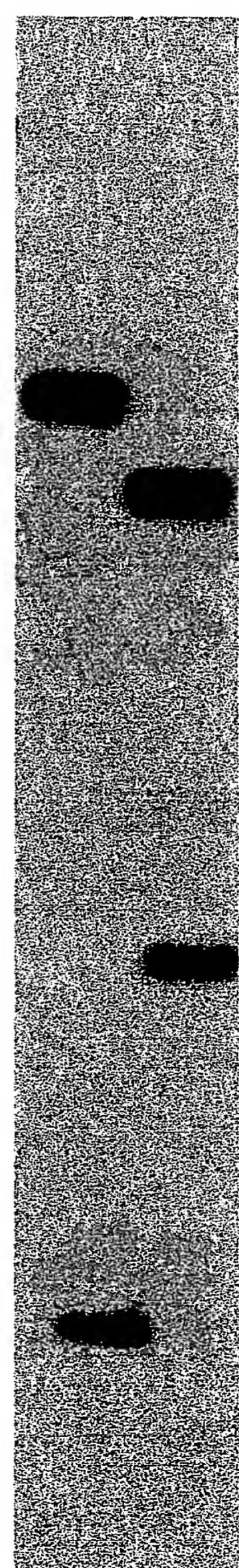
HC2A SSVV-----  
 KIAA -----  
 rat CVTLPHEPHVGTFCVMCKLRTTFRANHWF CQAQEEAMNGNGREKEPWTVI FNSRFYRSWGK  
 HC4 EVE-----  
 HC1 SAEV-----  
 HC3 -----  
 HC5 -----  
 HC2A -----  
 KIAA -----  
 rat VHIFF-----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

Fig. 6B (cont.)

0.000 0.001 0.002 0.003 0.004 0.005 0.006 0.007



genomic DNA



BAC 6 DNA

Fig. 7

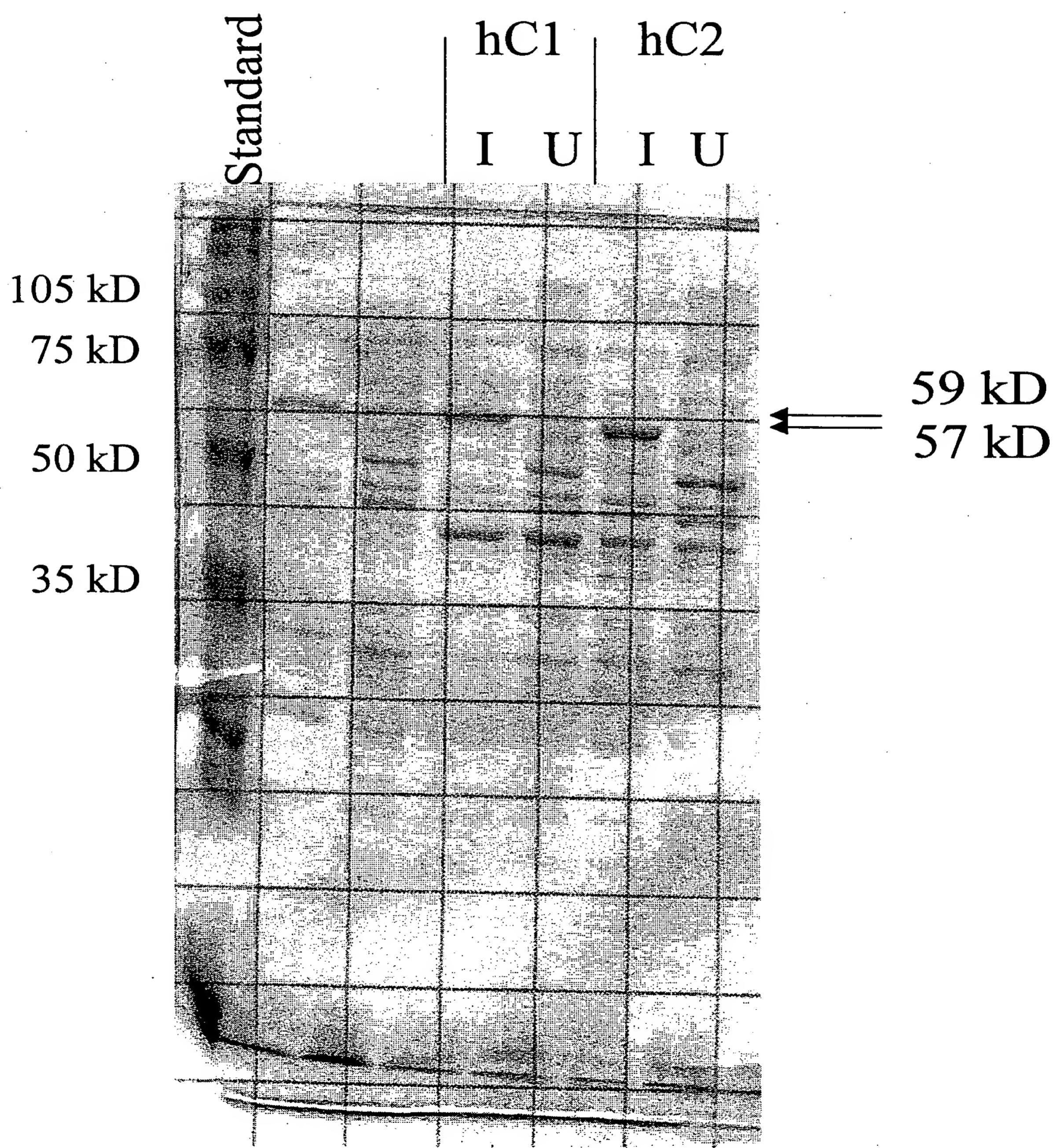


FIG. 8

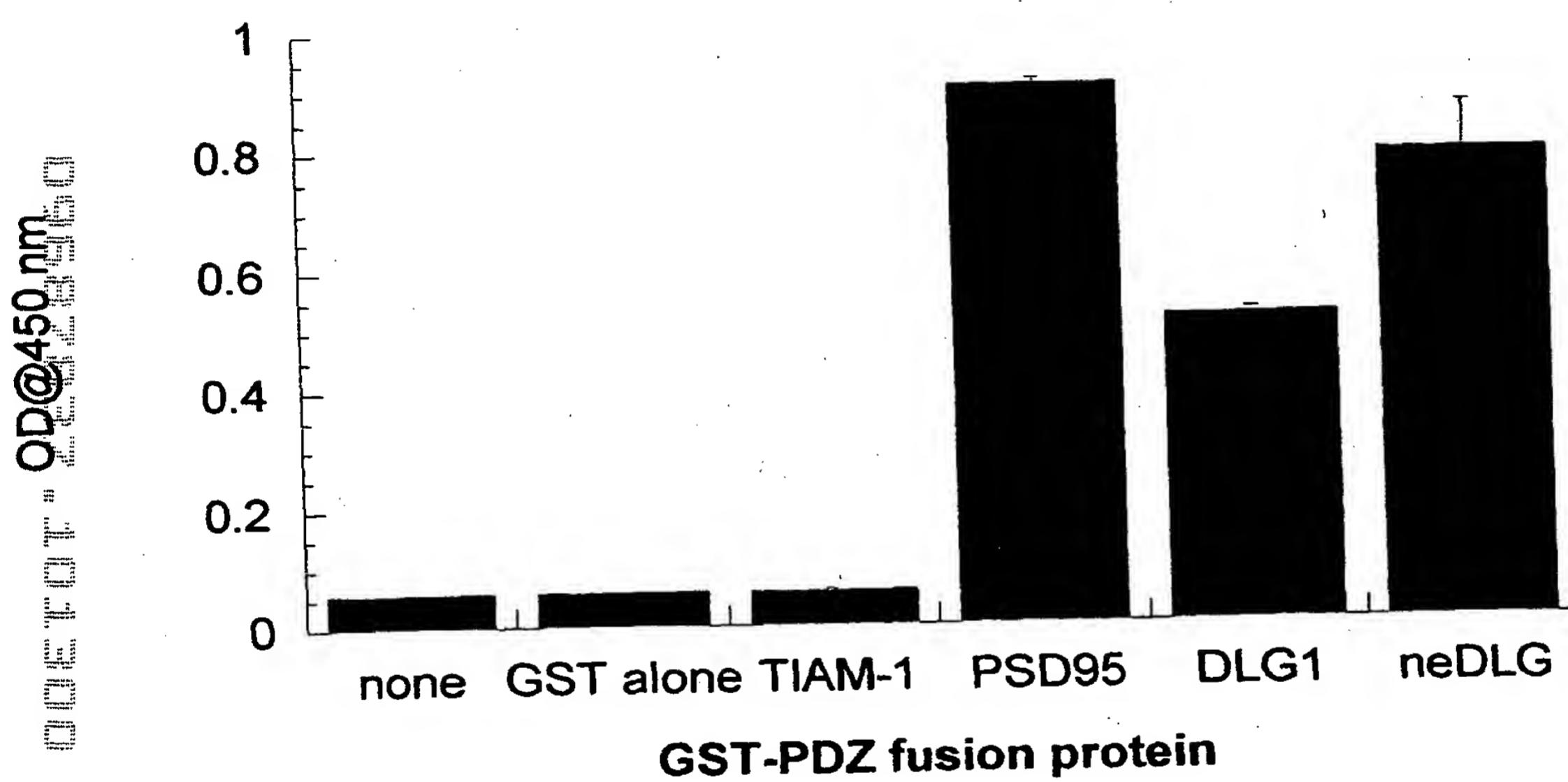


FIG. 9A

DLG1 NeDLG PSD95

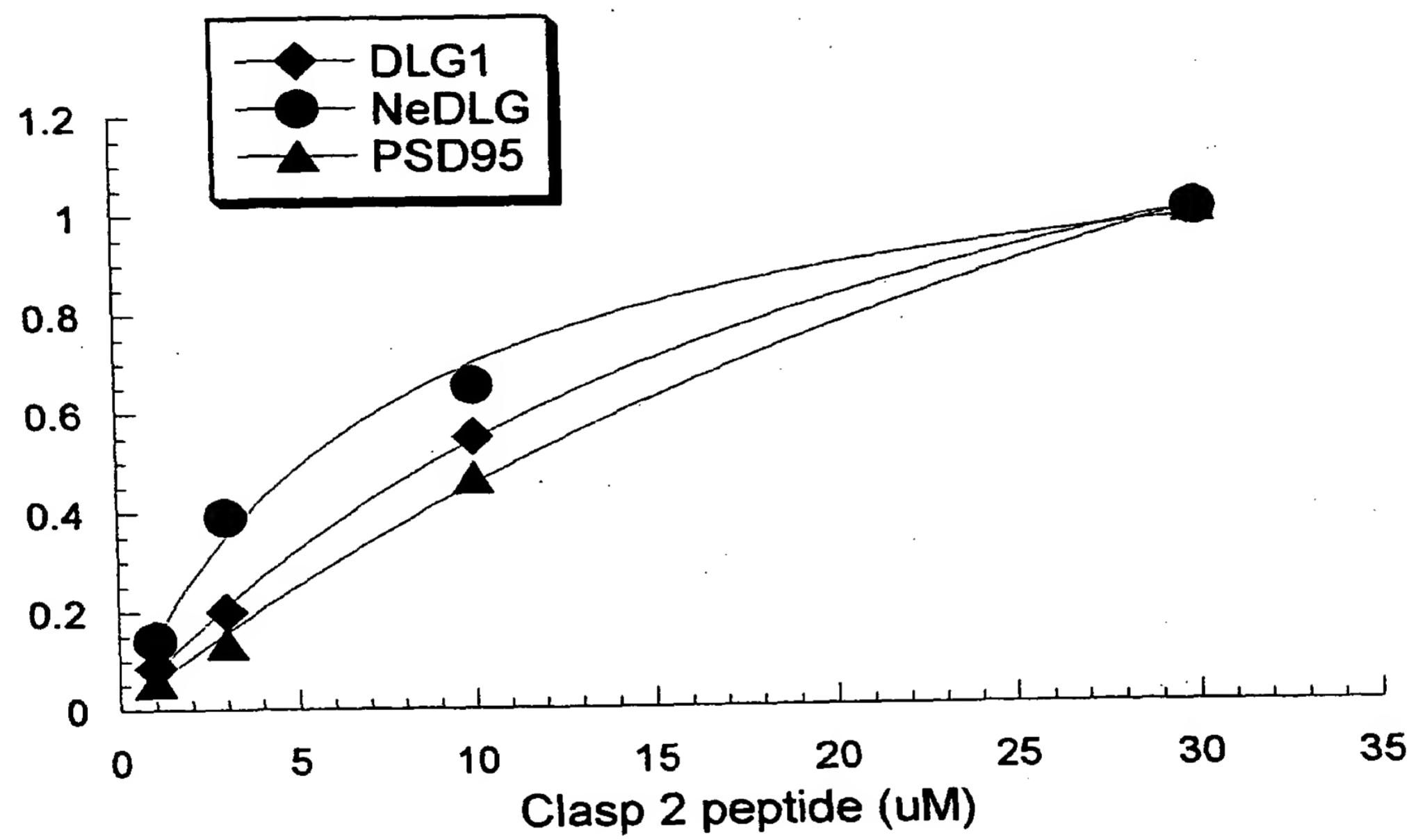


FIG. 9B

OD @ 450 nm

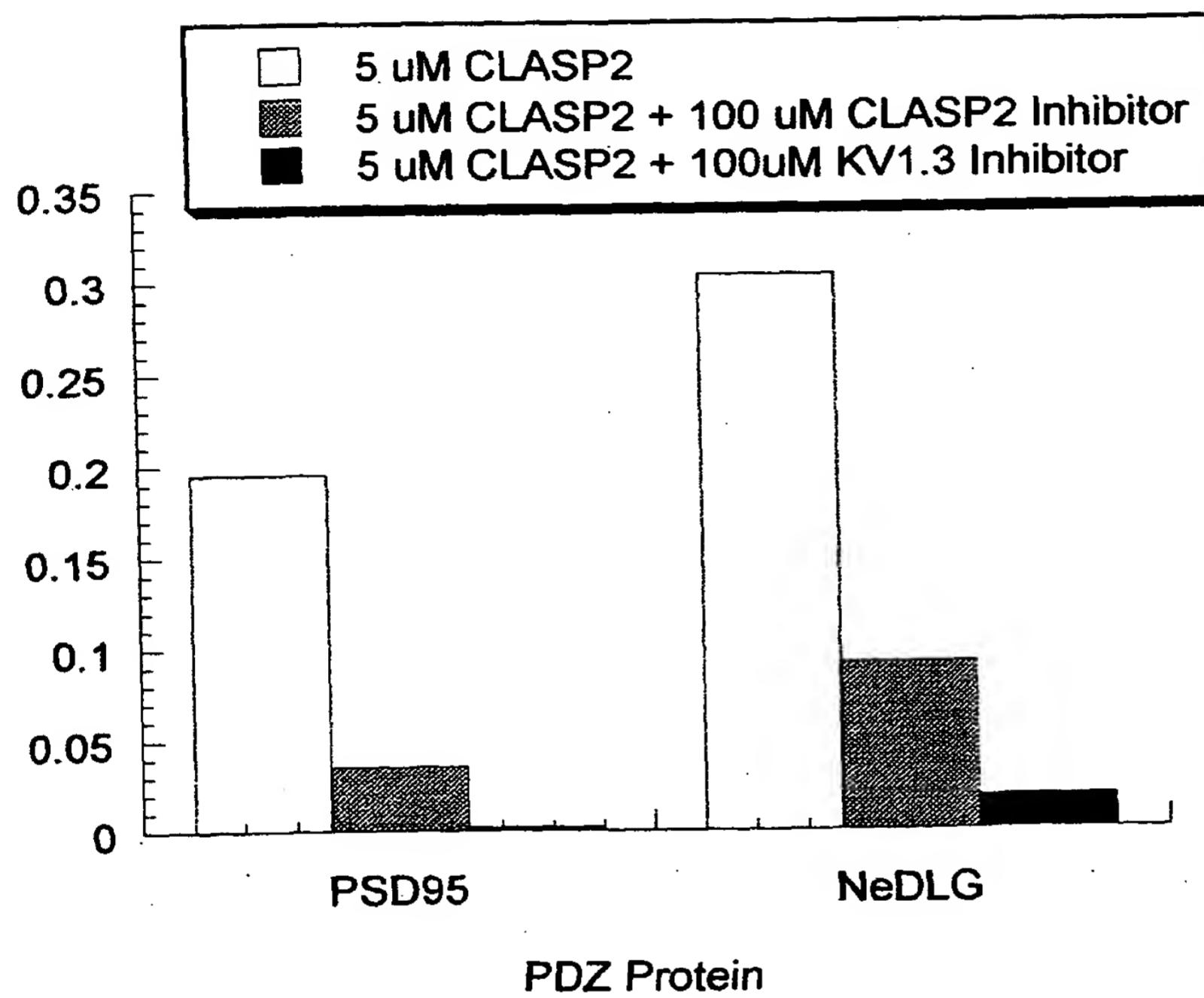


FIG. 9C

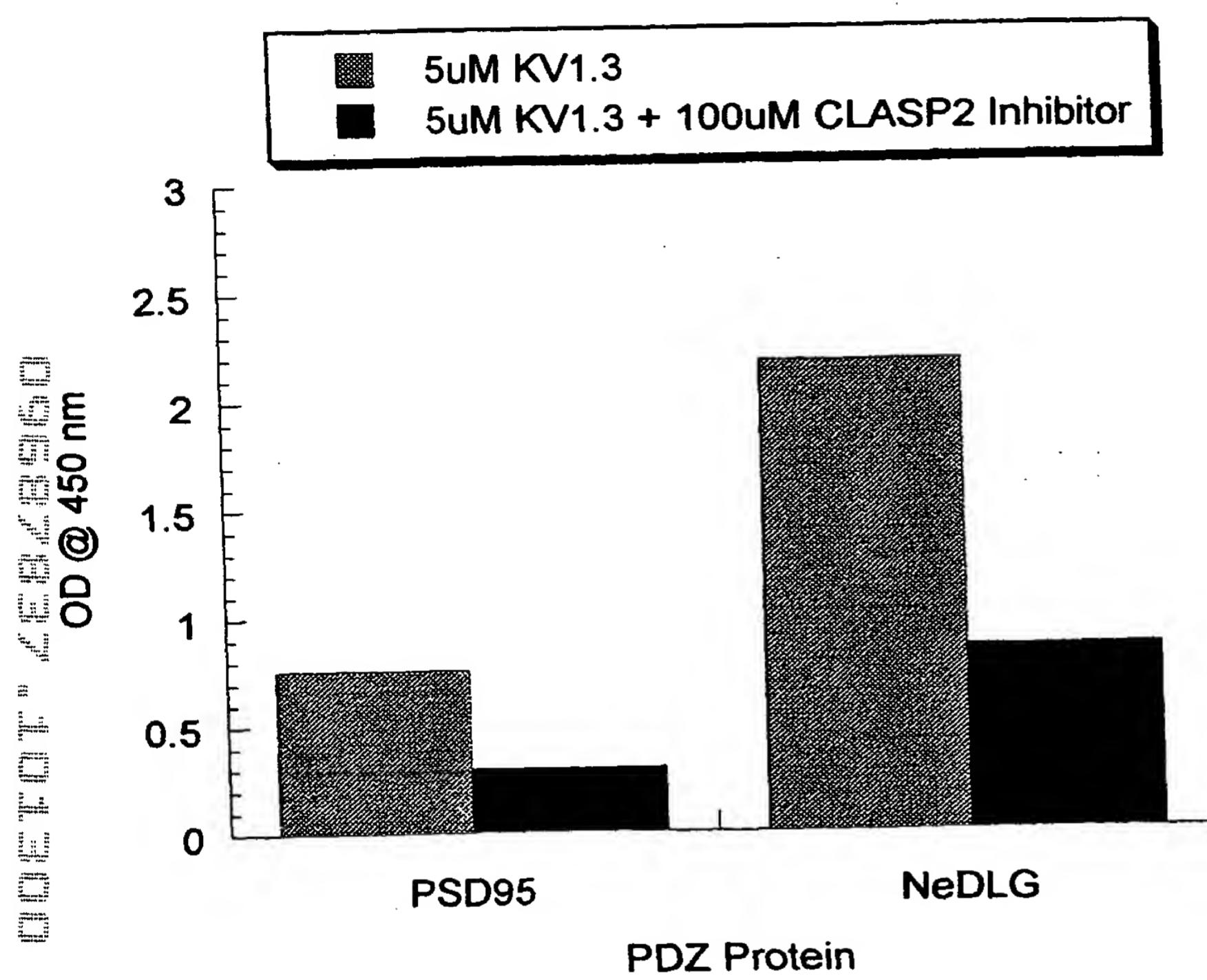


FIG. 9D

	10	20	30	40		50	60	70	80	
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG		GCCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA		TTTTATGATG	AGATTAATAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG		CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTGG	CTACTCCTGG	CTTCCCTCC		TGAAAGACGG	AAGGGTGGT	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTGGCG	AAACCTCCCT	CGGGCTATCT	TGGCTACCAA		GAGCTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAATAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTAAAAA	TTTCCACTCA		TCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA	480
481	ATTTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCA		ACCCCTAGGA	AACCGAACTTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCTA		CTATCCTAAA	CCAGCTGTC	CGAGTCCTCA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT		CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACCGCTATA	AGGCTGAGCC		ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCT	TCTGCCGATT		TCCTCACCAAG	CAACAAACTA	CTGAGGTA	CATGGTTTTT	880
881	CTTGTATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA		GAGAACTCCA	AAGTTAAGTT	GCTGCCAAC	CAGAGATTTC	960
961	CTGCATCCTA	TCATCATGCA	GGGGAAACCG	TTGTTAAATAT		GCTGATGCCA	CACATCACTC	AGAAGTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTTCTCA		TCAAGAGATG	TTTCAACCTTC	ATGGACAGGG	GCTTTGTCTT	1120
1121	CAAGCAGATC	AACAACATACA	TTAGCTGTTT	TGCTCTGG		GACCCAAAGA	CCCCTTTG	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTTC	CGTTGAACTT		ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA		GAAACCACCT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACGCCCTC	CAGGAGTTCC	GGGAGGTCGG	TCTGATGCC		ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC		CACCCCTCAC	CTGCTCTGT	TTGGCTGCT	GATTGAAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTC	CCCTTCCCTG		TGAACGCGGG	CATGACGTTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAAGC		ACCCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA		CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTGGGTAA	CAGCCTTCCA	GAAGGAATA		GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCCGTGG	TTCGCTGTGA	TAAACTTGAC		CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTACCA	1920
1921	TCTTAAAGAG	CATGTCTGAT	GATGCTTTGT	TTACATATTG		GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGA		AGCATAACAT	AGCCAGGAAC	CAGGAGGGGT	TTGGGACCCAT	2080
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT		AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2151	GCAGCCTGGA	TAACCTCTC	ACTTTAAC	ACAGCTATGG		CCACTCGGAC	GCAGATGTC	TGCACCAGTC	ATTACTGAA	2240
2241	GCCAACATTG	CTACTGAGGT	TTGCTCTGACA	GCTCTGGACA		CGCTTCTCT	ATTACATTG	GCGTTAAGA	ACCAGCTCCT	2320
2321	GGCGAACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT		GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2401	CGGTTTAAA	AAATGTCCTC	ACTGCCTTAA	GGTCCTTAAAT		TTATAAGTTT	CCCTCAACAT	TCTATGAGG	GAGAGCGGAC	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AACTGCTGTA		ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTG	TTACACTGGA		AAGAAGTCCT	TTGTCGGAC	ACATTGCAA	GTCATCATAT	2640
2641	CTGTCAAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGA		AACCAGATTG	CAGCAGTCCC	TGTCCATCAT	CAACAACTGT	2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT		CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGCT	2800
2801	AATGGCCACC	CCCCAGATGA	AGGAGCATGA	GAACGACCCA		GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	CCCCGAGCTC	AGGAAGACGT	GGCTCGACAG		CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG		AAATATCTCAC	ACGGAAAGGC	GTGTTAGAC	AAGGATGCAC	3040
3041	CGCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC		TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCAGCAGA		TGGACTCTGG	AAAGCCGAGC	GCTACGGAGCT	CATCGCCGAC	3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG		ATTTCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTCACAA	3280
3281	GGAAACCCAAA	CTCACACC	TGTCGAAAT	TTCTCAGAGA		CTCCTTAAAC	TGTACTCGGA	TAATTTGGT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCCTAAGGA		TCTGGATTCT	AAAGTATGCAT	ACATCCAGGT	GACTCACGTC	3440
3441	ATCCCCCTCT	TTGACGAAAAA	AGAGTTGCAA	GAAGGGAAAAA		CAGAGTTGAA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACCGAGA	CCGGGAAGAG	GCAGGGCGGG		GTGGAAGAGC	AGTGCACAAAGC	GCGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AGGAAGCGCA	TCCCTGTCAT		GTACCAAGCAC	CACACTGACC	TGAACCCAT	CGAGGTGGCC	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC		TGTGCTCTC	GGCGGAGGTG	GACATGATCA	AACTGCAGCT	3760
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGGT	CAATGTCAGC		CCACTAGCAT	ATGCGCGAGC	TTTCTTCA	GATAACAAAC	3840
3841	CAAAGCGATA	TCCGTACAAT	AAAGTGAAGC	TGCTTAAGGA		AGTTTTCAGG	CAATTTGTGG	AAGCTTGCAGG	TCAAGCTTAA	3920
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTGAGT		ATCAGGAAGA	ARTGAAAGCC	AACTACAGGG	AAATGGCGAA	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG		GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAAACAAGCA	CAATGTTCA		CGGGATGACC	AGCTCGTCTT	CGGTGTTGTTG	ATTACATCTC	4160
4161	ATGGCCCCTG	TGTGGGGACT	TGCTTGTCA	TTTGCAAACCT		CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG		AACAAACGTTA	TTTCTTAAACA	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTT	TAAATCTCAC	TGGCAATATT		CAAAGTTTCTC	ATTGTTGCTT	AAACAAGGTG	TGGTAGACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAAGAGTA		GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCC		GGGGACCTTT	TGCTCTGACT	CGTGCAGGAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG		TTGTATGACT	AGGAGTTGTC	CTATTATCTC	ATTCAACAAAC	4640
4641	ATAGAGCAAG	AATAGTGAAGC	TAATGAGACT	AGACACTCAA		TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TGTCATTAA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTA		CATTTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTAAAT	4800
4801	TGTGATAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT		TAATGGTTTA	TTCTTGTCA	AAAAATGTGC	AATATGGAGA	4880
4881	TGTGATAAT	TCTTACT							4898	

FIG. 10A

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIH	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK
81	SMTTILKPSA	DFLTSNKLLR	YSWFFF DVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHAAE	TVVNMLMPHI	TQKFGDNPEA
161	SKNA NHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPM PFG	KGRIQRYQDL
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTALQE	FREVRLIAIS	VLKNLLIXHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	WVRCDKLDQS	EIKSLLMCFL	YILKSMSSDA	LFTYWNKAST	SELMDFFTIS
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN
721	SDRLIKHTSF	SSDVVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDMSARIH	VRNGDLSEAA
801	MCYVHVTALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY
881	KLIPIYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEIISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLD SKY	AYIQVTHVIP
961	FFDEKE LQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLOGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV
	10	20	30	40	50	60	70	80

FIG. 10A (cont.)

	10	20	30	40
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG
81	GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA
161	ATGAAAAGCA	CCACCTGTG	CTCACATTCT	TCCATGTCAG
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTCC
321	CGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAAA	TTTCCACTCA
481	ATTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCA
561	CATGGGATGG	AAGGCCACGT	GATGATGCC	TTCTTGCCCA
641	ACAGGAAGAA	GTCGGGTTA	ACGTGACTCG	GGTCATTATT
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC
801	ACCAAATCCA	TEACCAAGGAT	TCTCAAGCT	TCTGCCGATT
881	CTTGATGTA	CTGATCAAT	CTATGGCTCA	GCATTGATA
961	CTGCATCTA	TCATCATGCA	GGGGAACCG	TTGTTAAATAT
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGCTTCA
1121	CAAGCAGATC	AACAACATACA	TTAGCTGTTT	TGCTCTGGA
1201	GTGAGTGTG	CAACCATGAA	CATTATATT	CGTTGAACCT
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATGCC
1441	ATGACAGATA	TGCTTCAGG	AGCCATCAGG	CAAGGATAGC
1521	GTCCAGCGGA	TCAATGTCAG	GGATGTTGTC	CCCTTCCCTG
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAAGC
1681	TCTCCGGCAT	TGCTTCCTCA	TATACAACCT	CAACTCCAAA
1761	ATAAGCACAG	ATTGGGTAA	CAGCCTTC	GAAGGAATA
1841	CACATTGGGA	AATTCCGTGG	TTCGCTGTA	AAAACCTGAC
1921	TCTTAAAGAG	CATGCTGAT	GATGCTTTGT	TTACATATTG
2001	ATATCTGAAG	TCTGCCGCA	CCAGTTCCAG	TACATGGGA
2081	AGTTCATGAT	CGAAAGCTC	AGACATTGCC	TGTTCCCGT
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTAAC	ACAGCTATGG
2241	GCCACACATTG	CTACTGAGGT	TTGCTGACA	GCTCTGGACA
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT
2401	CGGCTTTAAA	AAATGCTTC	ACTGCCCTAA	GGTCCTTAAT
2481	ATGTGTGCGG	CTCTGTTA	CGAGATTCTC	AAGTGTGTA
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTGTA	TTACACTGGA
2641	CTGTCAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGA
2721	GCCACACGTG	ACCGGCTTAT	TAAGCACAC	AGCTTCTCCT
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG
2961	GCAGCAATGT	GCTATGTC	CGTAACAGGC	CTAGTGGCAG
3041	CGCCTTCAGG	GTCTTACCC	CAAACATCGA	CGAGGAGGCC
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCGCAGA
3201	ATCTACAAAC	TTATCATCCC	CATITATGAG	AAGGGGAGGG
3281	GGAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCCTAAGGA
3441	ATCCCCCTCT	TTGACGAAAAA	AGAGTTGCAA	GAAGGGAAAAA
3521	TGAGATGCCA	TTTACGCGA	CCGGGAAGAG	GCAGGGCGGG
3601	TACACTGCTT	CCCTTATGTC	AAGAAGCGCA	TCCCTGTAT
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGGT	CAATGCTGGC
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAGGA
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA
4161	ATGGCCCGTG	TGTTGGGACT	TGCTTGTCA	TTTGCAAAC
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAG
4321	AGAAGGTGCA	CATATTTTT	AAATCTCAC	TGGCAATATT
4401	TCTTGAGCTG	GACTTAGATT	TTATTCCTCC	TTGCAAGAGA
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCC
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTC	TAGGAGTATG
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTA
4801	TGTGATAAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT
4881	TGTATACAAG	TCTTACT		

	50	60	70	80
50	GCCCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC
58	TTTATGATG	AGATTTAAAT	AGAGTTGCC	ACTCAGCTGC
66	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
74	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
82	GAGCTTGGGA	TGGCAGGCA	TTATGGTCCG	GAAATTAAAT
90	TCTGGTTCT	ACAGGGATAAC	TCAGGATCAG	CATTTACATA
98	AGCCTTAGGA	AACGAACITG	TAAAGTACCT	TAAGAGCTG
106	CTATCCTAAA	CCAGCTGTC	CGAGTCCCTCA	CCAGAGCCAC
114	CATGTGGTTG	CCCAGTGCC	TGAGGAAGGA	TTGGAGAGCC
122	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
130	TCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT
138	GAGAAGCTCA	AAGTTAAGTT	GCTGGAAAC	CAGAGATTT
146	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
154	TCAAGAGATG	TTTACCTTC	ATGGACAGGG	GCTTTGCTT
162	GACCCAAAGA	CCCTCTTGA	ATACAAGTT	GAATTCTCC
170	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA
178	GAAACCACTT	CTTGGGGGA	CTGTTACTGA	GGGAGGTGGG
186	ATCAGTGTG	TCAAGAACCT	GCTGATAAAAG	CATTCTTTG
194	CACCCCTCTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAC
202	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
210	ACCCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
218	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC
226	GTGAGAAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
234	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCCCTCTACA
242	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA
250	AGCGATAACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
258	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
266	CCACTCGGAC	GCAGATGTC	TGCACCACTC	ATTACTGAA
274	CGCTTCTCT	ATTTACATTG	GCGTTTAAGA	ACCAGCTCCT
282	GATGTCCTACC	TGTTTTCT	TCAAAAACAT	CAGTCIGAAA
290	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
298	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT
306	AAGAAGTCCT	TTGTCGGAC	ACATTGCAA	GTCATCATAT
314	AACCAGATTG	CAGCAGTCCC	TGTCCATCAT	CAACAACGT
322	CTGATGTA	GGACTTAACC	AAAAGGATAAC	GCACGGTGCT
330	GAGATGCTGG	TGGACCTCCA	GTACAGCTG	GCCAAATCCT
338	CATGGCCAGG	ATCCATGTC	AAAATGGCGA	TCTCTCAGAG
346	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC
354	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTCA
362	TGGACTCTG	AAAGCCGAGC	GCTACGAGCT	CATGCCGAC
370	ATTTCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTACAA
378	CTCCTTAAAC	TGTACTCGGA	TAATTTGGT	TCTGAAAATG
386	TCTGGATTCT	AACTATGCA	ACATCCAGGT	GACTCACGTC
394	CAGAGTTG	GAGATCCCAC	AACATCCGCC	GCTTCATGTT
402	GTGGAAGAGC	AGTGCACACG	GCGCACCATC	CTGACAGCCA
410	GTACCGAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
418	TGTGCTCTC	GGCCGAGGTG	GACATGATCA	AACTGAGCT
426	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAAACA
434	AGTTTCAGG	CAATTGTTG	AAGCTTGGCGG	TCAAGCCTTA
442	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
450	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCTC	CTTCACATCT
458	CGGGATGACC	AGCTCGTCTT	CGGTGCGTGTG	ATTACATCTC
466	CAGGATGCTT	TCCAAGCCA	ATCACTGGGG	AGACCGAGCA
474	AAACAACGTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
482	CAAAGTTTTC	ATTGTGTC	AAACAAGGTG	TGGTAGACAC
490	GTGTTAGAAT	AGATGGCTTA	CAGAAAAAAA	AGGTTCTGGG
498	GGGGACCTTT	TGCCCTCGACT	CGTGCCTGGAA	ATCTGATCGT
506	TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCAACAAAC
514	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TGTCATTAA
522	CATTTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTAAAT
530	TAATGGTTTA	TTCTTGTCA	AAAAATGTGC	AATATGGAGA

FIG. 10B

	10	20	30	40	50	60	70	80
1	MEGHVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK
81	SMITILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQHLIEN	SKVKLLRNQR	FPASYHAAE	TVVNMLMPHI	TQKFGDNPEA
161	SKNAHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPPFG	KGRIQRYQDL
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTLALQE	FREVRLIAIS	VLKNILLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNNS	VVRCDKLDQS	EIKSLLMCFL	YILKSMSSDA	LFTYWNKAST	SELMDFFTIS
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKVFDV	YLCFLQKHQS	ETALKNVFTA	IRSLIYKFPS	TFYEGRADMC
641	AALCYEILKC	CNSKLSSIRT	EASQQLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQQLIADV	VGIGETRFQQ	SLSIINNCAN
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDMSARIH	VKNGDLSEAA
801	MCYVHVTALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY
881	KLIPIYER	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDISKY	AYIQVTHVIP
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRGQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV
	10	20	30	40	50	60	70	80

### FIG. 1DB (cont.)

	10	20	30	40
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG
1	GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA
1	ATGAAAGCA	CCACCTGTG	CTCACATTCT	TCCATGTCAG
1	GTCGTTGAA	CCCAAGTGG	CTACTCCTGG	CTTCCCCCTCC
1	GGTCTCGGCG	AACCTCCCT	CGGGCTATCT	TGGCTACCAA
1	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAAA	TTTCCACTCA
1	ATTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGGCCA
1	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGGCCA
1	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT
1	ACTTGAGGTC	ATATGTTAAG	TACCGTATA	AGGCTGAGCC
1	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT
1	CTTTGATGTA	CTGATCAAAT	CTATGGCTA	GCATTTGATA
1	CTGCATCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT
1	GAGGCATCTA	AGAACCGGAA	TCATAGCCTT	GCTGTCCTCA
1	CAAGCAGATC	AACAACATACA	TTAGCTGTT	TGCTCCTGGA
1	GTGTAGTGTG	CAACCATGAA	CATTATATT	CGTTGAACCT
1	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA
1	GACAGCCCTC	CAGGAGTTTC	GGGAGGTCCG	TCTGATCGCC
1	ATGACAGATA	TGCTTCAGG	AGCCATCAGG	CAAGGATAGC
1	GTCCAGCGGA	TCAATGTGAG	GGATGTTGCA	CCCTTCCCTG
1	ACCAGCTGTG	AATCCGCTGG	TGACGCCGA	GAAGGGAAAGC
1	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA
1	ATAAGCACAG	ATTGGGTTAA	CAGCCTTCCA	GAAGGAAATA
1	CACATTGGGA	AATTCCGTGG	TTCGCTGTGA	TAAACTTGAC
1	TCTTAAAGAG	CAITGTCGTAT	GATGTTTGT	TTACATATTG
1	ATATCTGAAAG	TCTGCTGCA	CCAGTTCCAG	TACATGGGA
1	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT
1	GEAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG
1	GCACACATTG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA
1	GGCCGACCACAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT
1	CGGCTTTAAA	AAATGTCCTC	ACTGCCCTAA	GGTCCTTAAT
1	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTGTTA
1	GCTCTACTTC	CTGATGAGGA	ACAACTTGA	TTACACTGGA
1	CTGTCAGGCCA	GCTGATAGCA	GACGGTGTG	GCATTGGGAA
1	GCCAACAGTG	ACCGGTTAT	TAAGCACACC	AGCTTCTCCT
1	ATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA
1	ATGCCAGCAC	GCCCCAGCTC	AGGAAGACGT	GGCTCGACAG
1	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG
1	CGCCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC
1	ACGAGGATGT	GCTGATGGAG	CTCCCTGAGC	AGTGGCGCAGA
1	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG
1	GGAAACCCAAA	CTCACACCCTC	TGTGGAAAT	TTCTCAGAGA
1	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCCTAAGGA
1	ATCCCCCTCT	TTGAGGAAA	AGAGTTGCAA	GAAGGAAAAA
1	TGAGATGCCA	TTTACGCAGA	CGGGGAAGAG	GCAGGGGGGG
1	TACACTGCTT	CCCTTATGTG	AAGAACGCA	TCCCTGTCAT
1	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGGAG	CTCOGGCAGC
1	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAGGT	CAATGCTGGC
1	CAAAGCGATA	TTCTGACAAAT	AAAGTGAAGC	TGCTTAAGGA
1	GCGGTAAACG	AACGTCGTAT	TAAAGAAGAC	CAGCTCGAGT
1	GGAGCTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG
1	TCAACGCCAT	CAGTGGGACT	CCAACAGCA	CAATGGTCA
1	ATGGCCCGTG	TGTGGGGACT	TGCTTGTCA	TTTGCCTAACT
1	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG
1	AGAAGGTGCA	CATATTTTT	TAAATCTCAC	TGGCAATATT
1	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAAGAGTA
1	ATCTACATGG	CAGGGAGGGC	TGCACGTACA	TTGATGCTTG
1	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG
1	ATAGAGCAAG	AATAGTGTG	TAACTGAGCT	AGACACTCAA
1	TCATCGACTC	CGGGACGGTC	ATATAATGTAT	TACATTCTA
1	TGTGATAAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT
1	TGTATACAG	TCTTACT		

	50	60	70	80
1	GCCCCCCCTC	GAGGTGCGACG	GTATCGATAA	GCTTGATATC
1	TITTTATGATG	AGATTTAAAT	AGAGTTGCCC	ACTCAGCTGC
1	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT
1	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
1	GAGCTTGGGA	TGGCAGGCA	TTATGGTCCG	GAAATTAAT
1	TCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA
1	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
1	CTATCTAAA	CCAGCTGTC	CGAGTCTCA	CCAGAGCCAC
1	CATGGGGTGT	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
1	ATATGTTGCC	TCTGAATACA	AGACAGTGC	TGAAGAACTG
1	TCCTCACCAG	CAACAAACTA	CTGAGGTA	CATGGTTTT
1	GAGAACTCCA	AAGTTAAGT	GCTGCGAAC	CAGAGATTC
1	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
1	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTGTCTT
1	GACCCAAAGA	CCCTCTTGA	ATACAAGTTT	GAATTCTCC
1	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATAACCA
1	GAAACCACIT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
1	ATCAGTGTG	TCAAGAACCT	GCTGATAAAG	CATTCTTTG
1	CACCCCTCTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAC
1	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
1	ACCCCTGGACA	ACAGCTGCA	CAAGGACCTG	CTGGGCGCCA
1	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC
1	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
1	CAGTCTGAGA	TTAAGAGCT	ACTGATGTG	TTCTCTACAA
1	GAACAAAGGT	TCAACATCTG	AACTTATGGA	TTTTTTACA
1	AGCGATAACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
1	AACAGAACAG	GAATGATGCA	TCGCAGATTG	CAGCAGCTGG
1	CCACTCGGAC	GCAGATGTC	TGCACCAGTC	ATTACTGAA
1	CGCTTTCTCT	ATTACATTTG	GGTTTAAGA	ACCAGCTCT
1	GATGTCCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
1	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCAGAC
1	ACTCCAAGCT	GAGCTCCATC	AGGACCGAGG	CCTCCCAAGCT
1	AAGAAGTCCT	TTGTCGGAC	ACATTTCGAA	GTCATCATAT
1	AACCAGATTC	CAGCAGTC	TGTCATCAT	CAACAACGT
1	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGT
1	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATTCCT
1	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTAGAG
1	AATATCTCAC	ACGGAAAGGC	GTGTTAGAC	AAGGATGAC
1	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTCA
1	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCCCGAC
1	ATTCTTTGTA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
1	CTCCCTAAAC	TGTACTCGGA	TAAATTGGT	TCTGAAAATG
1	TCTGGATTCT	AAAGTATGCA	ACATCCAGGT	GACTCACGTC
1	CAGAGTTTGA	GAGATCCCAC	AAACATCCGAC	GCCTCATGTT
1	GTGGAAGAGC	AGTGCACACG	GOGCACCATC	CTGACAGCCA
1	GTACCCAGC	CACACTGACC	TGAACCCAT	CGAGGTGGCC
1	TGTGCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCRAGCT
1	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
1	AGTTTTCAGG	CAATTGTTGG	AAGCTTGGG	TCAAGCCTTA
1	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
1	GAGGAGAAGA	CGAGCGTCCT	ACCGAATTCC	CTTCACATCT
1	CGGGATGAC	AGCTCGTCTT	CGGTCTGCTG	ATTACATCTC
1	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
1	AACAACTTAA	TTTCTTAACA	GACTTCTAT	AGGAGTGTGA
1	CAAAGTTTTC	ATTGTCATCT	AAACAAAGGTG	TGGTAGACAC
1	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
1	GGGGACCTTT	TGCCTCGACT	CGTGCCTGAA	ATCTGATGTT
1	TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCACAAAC
1	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCATTA
1	CAITTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTTAAT
1	TGTGATAAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT
1	TGTATACAG	TCTTACT		

	50	60	70	80
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FIG. 10C

	10	20	30	40	50	60	70	80	
MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV		VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	
SMITILKPSA	DFTLSNKLLR	YSWFDFDVL	KSMAQHLLIEN		SKVILLRNQR	FPASYHAAE	TVVNMLMPHI	TQKPGDNFEA	
SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP		KLFEYKFEF	LRVVCNHEHY	IPLNLPMPPFG	KGRIQRYQDL	
QDYSLTDEF	CRNHFLVGLL	LREVGTALQE	FREVRLIAIS		VLKNLLIKHS	FDDRYASRSH	QARLATLYLP	LFGLLIENVQ	
RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL		DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS	
TDSGNSLPER	NSEKSNSLDK	HQQSSTLGN	VVRCDLQDS		EIKSLLMCFL	YILKSMSSDA	LFTYWNKAST	SELMDFFTIS	
EVCLHQFQYM	GKRYIARNQE	GLGPIVHDK	SQTLPVSRNR		TGMMHARLQQ	LGSLDONSITF	NHSYGHSDAD	VLHQSLLEAN	
IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKVFDV		YLCFLQKHQS	ETALQNVFTA	LRSILYKFPS	TFYEGRADMC	
AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK		SFVRTHILOVI	ISVSQQLADV	VGIGETRPOQ	SLSIINNCAN	
SDRLIKHTSF	SSDVKDLTKR	IRTIVLMATAQ	MKEHENDPEM		LVDLQYSLAK	SYASTPELRK	TWLDMSARIH	VNGDLSEAA	
MCYVHVTALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM		MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	
KLIIPYIEKR	RDFFEDEDGK	EYTYKEPKLT	PLSEISQRLL		KLYSDKFGSE	NVKMIQDSGK	VNPFDLDSKY	AYIQVTHVIP	
FFDEKELOER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE		EQCKRRTILT	AIHCFFYVKK	RIPVMYQHHT	DLNPIEVAID	
EMSKVVAELR	QLCSSAEVDM	IKLOLKLOGS	VSVQVNAGPL		AYARAFLEDT	NTKRYPDNKV	KLKEVFRQP	VEACGQALAV	
NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEOICPLEE		KTSQLPNSLH	IFNAISGPT	STMVHGMTSS	SSVV	
	10	20	30	40		50	60	70	80

FIG. 10C (cont.)

	10	20	30	40
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG
81	GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA
61	ATGAAAAGCA	CCACCTGTG	CTCACATTCT	TCCATGTCAG
41	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTCC
21	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA
01	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA
81	ATTTTTCCA	GTACTGTCA	AAAACCGAAT	CTGGAGGCCA
61	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGGCCA
41	ACAGGAAGAA	GTGCGGGTTA	ACGTGACTCG	GGTCATTATT
21	ACTTGAGGTC	ATATGTTAAG	TACCGTATA	AGGCTGAGCC
01	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT
81	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA
961	CTGCATCCCA	TCATCATGCA	GCGGAAACCG	TTGTAATAT
041	GAGGCATCTA	AGAACCGGAA	TCATAGCCTT	GCTGTCTTCA
121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGAA
201	GTGTAGTGTG	CAACCCATGAA	CATTATATTG	CGTTGAACCTT
281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC
1441	ATGACAGATA	TGCTTCAGG	AGCCATCAGG	CAAGGATAGC
1521	GTCCAGCGG	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAAGC
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAAACCT	CAACTCCAAA
1761	ATAAGCACAG	ATTGGGGTAA	CAGCCTTCCA	GAAAGGAATA
1841	CACATTGGGA	AATTCCGTTG	TTGCGTGTGA	TAAACTTGAC
1921	TCTTAAAGAG	CAITGCTGTAT	GATGTTTGT	TTACATATTG
2001	ATATCTGAAAG	TCTGCTTGCA	CCAGTTCCAG	TACATGGGA
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG
2241	GCAACATTG	CTACTGAGGT	TTGCTTGACA	GCTCTGGACA
2321	GGCGGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTT
2401	GGGCTTTAAA	AAATGTCCTC	ACTGCTTAA	GGTCTTAAAT
2481	ATGIGTGCCTG	CTCTGTTTA	CGAGATTCTC	AAGTGCTGTA
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTGA	TTACACTGGA
2641	CTGTCAGGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGA
2721	GCCRACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCT
2801	AATGGCCACC	GCCCAGATGA	AGGACATGA	GAACGACCCA
2881	ATGCCAGCAC	GCCCCAGCTC	AGGAAGACGT	GGCTCGACAG
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG
3041	CGCCCTTCAGG	GTCATTACCC	CAAACATGA	CGAGGAGGCC
3121	ACGAGGATGT	GCTGATGGAG	CTCCCTGAGC	AGTGGCGAGA
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG
3281	GGAAACCCAAA	CTCACACCGC	TGTCGAAAT	TTCTCAGAGA
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCCTAAGGA
3441	ATCCCCCTCT	TTGACGAAA	AGAGTTGCAA	GAAAGGAAAA
3521	TGAGATGCCA	TTTACGAGA	CGGGGAAGAG	GCAGGGCGGG
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCTGTCAT
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCGGGCAGC
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC
3841	CAAAGCGATA	TCTGACAAAT	AAAGTGAAGC	TGCTTAAGGA
3921	GCGGTAAACG	AACGTCGTAT	TAAGAAAGAC	CAGCTCGAGT
4001	GGAGCTTCT	GAATCATGC	ATGAGCAGAT	CTGCCCCCTG
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAAGCA	CAATGGTCA
4161	ATGGCCCGTG	TGTTGGGACT	TGCTTGTCA	TTTGCAAAC
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG
4321	AGAAGGTGCA	CATATTTTT	AAAATCTCAC	TGGCAATATT
4401	TCTTGAGCTG	GACTTAGATT	TTATTCCTCC	TTGCGAGAGA
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTG
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA
4721	TCATCGACTC	CGGGACGGTC	ATATAATGTAT	TACATTTCTA
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT
4881	TGTATACAAG	TCTTACT		

	50	60	70	80
	GCCTCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC
	TTTATGATG	AGATTAAAAT	AGAGTTCGCC	ACTCAGCTGC
	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
	GAGCTTGGGA	TGGCAGGCCA	TTATGGTCG	GAATTTAAAT
	TCTGGTTCT	ACAGGGATAAC	TCAGGATCAG	CATTACATA
	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
	CTATCCTAAA	CCAGCTGTC	CGAGTCTCA	CCAGAGCCAC
	CATGTGGTGT	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
	TCCTCACCAG	CAACAAACTA	CTGAGGTA	CATGGTTTT
	GAGAACTCCA	AAGTTAAGT	GCTGCCAAAC	CAGAGATTT
	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT
	GACCCAAAGA	CCCTTCTTGA	ATACAAGTT	GAATTCTCC
	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATAACAA
	GAAACCACCT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
	ATCAGTGTG	TCAAGAACCT	GCTGATAAAG	CATTCTTTG
	CACCCCTCTAC	CTGCTCTGT	TGGTCTGCT	GATTGAAAAC
	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
	ACCCCTGGACA	ACAGCTGCA	CAAGGACCTG	CTGGGCGCCA
	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC
	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AAACAAAGTAG
	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
	GRACIAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTACA
	AGCGATAACAT	AGCAGGAAC	CAGGAGGGGT	TGGGACCCAT
	AAACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
	CCACTCGGAC	GCAGATGTG	TGCACCAAGTC	ATTACTTGAA
	CGCTTTCTCT	ATTACATTTG	GOGTTAAGA	ACCAGCTCT
	GATGTCCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
	ACTCCAAGCT	GAGTCCCATC	AGGACGGAGG	CTCCCAAGCT
	AAGAAGTCCT	TTGTCGGAC	ACATTGCAA	GTATCATAT
	AACCAGATTC	CAGCAGTCCC	TGTCATCAT	CAACAACIGT
	CTGATGTGAA	GGACTTAAACC	AAAAGGATAC	GCACGGTGT
	GAGATGCTGG	TGGACCTCCA	GTACAGCTG	GCCAAATCT
	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG
	AATATCTCAC	ACGGAAAGGC	GTGTTAGAC	AAGGATGACAC
	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTCA
	TGGACTCTGG	AAAGCCGAGC	GCTACAGACT	CATOGCCGAC
	ATTTCCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
	CTCCCTAAAC	TGTACTCGGA	TAATTTGGT	TCTGAAAATG
	TCTGGATTCT	AAGTATGCA	ACATCCAGGT	GACTCACGTC
	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT
	GTGGAAGAGC	AGTCAAACG	GCGCACCAC	CTGACAGCCA
	GTACAGCAC	CACACTGACC	TGAACCCAT	CGAGGTGGCC
	TGIGCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
	CCACTAGCAT	ATGCGCGAGC	TTTCTTGTAGAT	GATAACAAACA
	AGTTTTCAGG	CAATTGTTGG	AAGCTTGGGG	TCAAGCTTAA
	ATCAGGAAGA	AAATGAAAGCC	AACTACAGGG	AAATGGCGAA
	GAGGAGAAGA	CGACGCGTCTT	ACCGAATTCC	CTTCACATCT
	CGGGATGAC	AGCTCGTCTT	CGGTCGTGTG	ATTACATCTC
	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
	AAACAAACGTTA	TTTCTTAAACA	GACTTTCTAT	AGGAGTTGTA
	CAAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC
	GTGTTAGAAT	AGATGGCTA	CAGAAAAAAA	AGGTTCTGGG
	GGGGACCTTT	TGCTCGACT	CGTGCCTGAA	ATCTGATGTT
	TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCAACAAAC
	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTAA
	CATTTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTAAAT
	TAATGGTTTA	TTCTTGTCT	AAAAATGTGC	AAATATGGAGA

	10	20	30	40	50	60	70	80
	10	20	30	40	50	60	70	80
								4898

	10	20	30	40
MEGHVUMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIV	
SMTTILKPSA	DFLTSNKLLR	YSWFFFVDVLI	KSMAQHILIE	
SKNAHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	
QLDYSLTDEF	CRNHFLVGLL	LREVGTALQE	FREVRLIAIS	
RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	
TDSGNSLPER	NSEKNSLDK	HQSSSTLGNS	VVRCDKLDQS	
EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRA	SQTLPVSRNR	
IATEVCLTAL	DTLSLFTLAF	KNOLLADHGH	NPLMKKVF DV	
AALCYEILKC	CNSKLSSIRT	EASQLLYPLM	RNNFDYTGKK	
SDRLLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	
MCYVHVTALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	
KLIPIPIYEKR	RDFFEDEDGK	EYTYKEPKLT	PLSEISQRLL	
FFDEKELOER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGV	
EMSKKVAELR	QLCSSAEVDM	IKLQLKLOGS	VSVQVNAGPL	
NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	
	10	20	30	40

	50	60	70	80
VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80
SKVKLLRNQR	FPASYHAAE	TVVNMLMPHI	TQKFGDNPEA	160
KTLFEYKFEF	LRRVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ	320
DNSLHKDLIG	AISGLASPYT	TSTPNINSVR	NADSRGSLIS	400
EIKSLLMCFL	YILKSMSSDA	LFTYWNKAST	SELMDFPTIS	480
TGMMHARLQQ	LGSLDNLSTF	NHSYGHSDAD	VLHQSLLEAN	560
YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640
SFVRTHLQVI	ISVSQOLIADV	VGIGETRFQQ	SLSIINNCAN	720
LVDLQYSLAK	SYASTPELRK	TWLDMSARIH	VINGDLSEAA	800
MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELLIADIV	880
KLYSDKFGSE	NVIMIQDSGK	VNPIDLDSKY	AYIQVTHVIP	960
EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
AYARAFLDDT	NTKRYPDNKV	ILLKEVFRQF	VEACGQALAV	1120
KTSLVLPNSLH	IFNAISGPT	STMVHGMTSS	SSVV	1194
	50	60	70	80

故其子曰：「吾父之子，其名何也？」

FIG. 10D (cont.)

	10	20	30	40
AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	
GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	
ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCA	
GTCGTGAAA	CCCAGTTGG	CTACTCCGG	CTTCCCCCTCC	
GGTCTCGCG	AACTTCCCT	CGGGCTATCT	TGGCTACCAA	
GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCACTCA	
ATTTTTCCA	GTACTGTCAG	AAAACCGAA	CTGGAGGCCA	
CATGGATGG	AAGGCCACGT	GATGATGCC	TTCTTGCCCC	
ACAGGAAGAA	GTCGGGTTA	ACGTGACTCG	GGTCATTATT	
ACTTGAGGTC	ATATGTAAG	TACGCGTATA	AGGCTGAGCC	
ACCAAATCCA	TGACCACGAT	TCTCAAGCT	TCTGCCGATT	
CITTGATGTA	CTGATCAAT	CTATGGCTCA	GCATTGATA	
CTGCATCTA	TCATCATGCA	GCGGAAACCG	TITGAAATAT	
GAGGCATCTA	AGAACGGAA	TCATAGCTT	GCTGCTTCA	
CAAGCAGATC	AACAATACA	TTAGCTGTT	TGCTCTGGGA	
GTTGAGTGTG	CAACCATGAA	CATTATATTC	CGTGAACCT	
GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	
GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATGCC	
ATGACAGATA	TGCTTCAGG	AGCCATCAGG	CAAGGATAGC	
GTCCAGCGGA	TCATGTGAG	GGATGTGTC	CCCTTCCCTG	
ACCAAGCTGTG	AATCCGCTGG	TGACGCGCA	GAAGGGAAAGC	
TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	
ATAAGCACAG	ATTGGGTAA	CAGCTTCCA	GAAGGAAATA	
1 CACATTGGGA	ATTTCGGG	TTCGCTGTA	AAAACCTGAC	
1 TCTTAAAGAG	CATGCTGAT	GATGTTTGT	TTACATATTG	
1 ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGA	
1 AGTTCATGAT	CGAAAGCTC	AGACATGCC	TGTTTCCCGT	
1 GCAAGCTGGA	TAACTCTCTC	ACTTTAAC	ACAGCTATGG	
1 GCCACACATTG	CTACTGAGGT	TTGCCATGACA	GCTCTGGACA	
1 GGCGGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT	
1 CGGCTTAA	AAATGCTTCA	ACTGCCAA	GGTCTTAAT	
1 ATGGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTGTA	
1 GCTCTACITC	CTGATGAGGA	ACAACCTTGA	TTACACTGGGA	
1 CTGTCAGGCCA	GCTGATAGCA	GACGTGTTG	GCATTGGGG	
1 GCGAACAGTG	ACCGGTTAT	TAAGCACACC	AGCTTCTCT	
1 AATGCCACC	GGCCAGATGA	AGGAGCATGA	GAACGACCCA	
1 ATGECAGCAC	GGCCGAGCTC	AGGAAGACGT	GGCTCGACAG	
51 GCAQCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	
11 CGCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC	
21 ACGAGGATGT	GCTGATGGAG	CTCCCTGAGC	AGTGCAGCAGA	
01 ATATCACAAAC	TTATCATCCC	CAITTATGAG	AAGCGGAGGG	
81 GGAACCCAAA	CTCACACCCG	TGTCGGAAT	TTCTCAGAGA	
61 TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	
41 ATCCCCCTCT	TTGACGAAA	AGAGTTGCAA	GAAGGAAAAA	
21 TGAGATGCCA	TTTACCGAGA	CCGGGAAGAG	GCAGGGGGGG	
01 TAGACTGCTT	CCCTTATGTC	ARGAAGCGCA	TCCCCTGTCAT	
81 ATTGAGGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	
61 CAAACTCCAG	GGCAGCGTGA	GTGTCAGGT	CAATGCTGGC	
141 CAAAGCGATA	TCCGACAAAT	AAAGTGAAGC	TGCTTAAGGA	
21 GCGGTAACG	AACGTCTGAT	TAAGAAGAC	CAGCTGAGT	
01 GGAGCTTCT	GAATCATGC	ATGAGCAGAT	CTGCCCCCTG	
081 TCAACGCCAT	CAGTGGGACT	CCAAACAAGCA	CAATGGTTCA	
161 ATGGCCCGTG	TGTGGGACT	TGCTTGTCA	TTTGCAAACT	
241 CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	
321 AGAAGGTGCA	CATATTTTT	TAATCTCAC	TGGCAATATT	
601 TCTTGAGCTG	GACTTAGATT	TTATCTTCC	TTGCAAGAGTA	
881 ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCCTG	
561 AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG	
641 ATAGAGCAAG	AAATGTGAGC	TAACTGAGCT	AGACACTCAA	
721 TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCCTA	
801 TGTGATAAAT	TGTGCTGGT	CCAGTATATG	CAATACACTT	
881 TGTATACAG	TCTTACT			

	50	60	70	80
GCCCCCCCCC	GAGGTGACG	GTATCGATAA	GCTTGTATTC	80
TTTATGATG	AGATTTAAAT	AGAGTTGCC	ACTCAGCTGC	160
CTGTGACAAC	TCAAGTAAAG	GAAGCAGCGA	GAAGAGGGAT	240
TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
GAGCTTGGGA	TGGGCAGGCA	TTATGGTCG	GAATTTAAAT	400
TCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCG	560
CTATCCTAA	CCAGCTGTC	CGAGTCCTCA	CCAGAGCCAC	640
CATGTGGT	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
TCCTCACAG	CAACAAACTA	CTGAGGTACT	CATGGTTTT	880
GAGAACTCCA	AAGTTAAGTT	GCTGCGAAC	CAGAGATTC	960
GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
TCAAGAGATG	TTCACCTTC	ATGGACAGGG	GCTTGTCTT	1120
GACCCAAAGA	CCCTCTTGA	ATACAAGTT	GAATTTCTCC	1200
ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA	1280
GAACCAACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
ATCAGTGTG	TCAAGAACCT	GCTGATAAAG	CATTCTTTG	1440
CACCCCTCTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAC	1520
TGAACGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
ACCCGGACCA	ACAGCTGCA	CAAGGACCTG	CTGGGCGCCA	1680
CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC	1760
GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
CAGTCTGAGA	TTAAGAGCCT	ACTGATGTT	TTCTCTTACA	1920
GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA	2000
AGCGATACAT	AGCCAGGAAC	CAGGAGGGT	TTGGACCCAT	2080
AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
CCACTCGGAC	GCAGATGTC	TGCACCACTC	ATTACTTGA	2240
CGCTTCTCT	ATTTACATTG	GCGTTTAAGA	ACCAGCTCT	2320
GATGCTTAC	TGTTTTCT	TCAAAACAT	CAGTGTGAAA	2400
TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC	2480
ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAAGCT	2560
AAGAAGTCTT	TGTCGGAC	ACATTGCAA	GTCACTCATAT	2640
AACCAAGATTC	CAGCAGTCCC	TGTCATCAT	CAACAATGT	2720
CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGT	2800
GAGATGCTGG	TGGACTCTCA	GTACAGCTG	GCCAAATCT	2880
CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
AATATCTCAC	ACGGAAAGGC	GTGTTAGAC	AAGGATGAC	3040
TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTCA	3120
TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCGAC	3200
ATTTCCTTGA	AGATGAGAT	GGAAAGGAGT	ATATTACAA	3280
CTCCCTAAAC	TGTACTCGGA	TTAATTGGT	TCTGAAAATG	3360
TCTGGATTCT	AAGTATGAT	ACATCCAGGT	GAATCCAGTC	3440
CAGAGTTGAA	GAGATCCCAC	AAACATCCGCC	GCCTCATGTT	3520
GTGGAGAGC	AGTCAAACG	GGCACACATC	CTGACAGCCA	3600
GTACCAAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3680
TGTGCTCTC	GGCGGAGGTG	GACATGATCA	AACTGCAGCT	3760
CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3840
AGTTTCAGG	CAATTGTTG	AAAGCTTGGG	TCAAGCTTA	3920
ATCAGGAAGA	AATGAAAGCC	AAACTACAGGG	AAATGGCGAA	4000
GAGGAGCTT	CGAGCGTCTT	ACCGAAATTCC	CTTCACATCT	4080
CGGGATGACC	AGCTCGTCTT	CGGTGCGTGTG	ATTACATCTC	4160
CAGGAATGCTT	TCCAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
AACAACTGTTA	TTTCTTAACA	GACTTTCTAT	AGGAGTGTGA	4320
GTGTTAGAAT	AGATGCGCTA	CAGAAAAAAA	AGGTTCTGGG	4400
GGGGACCTTT	TGCTCGACT	CGTGCCTGAA	ATCTGATGTT	4480
TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCAACAC	4560
TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TGTCATTAA	4640
CATTTTAAT	ACTCACATGG	GCTTATGCTAT	TAAGTTAAAT	4720
TGTGATAAAT	TGTGCTGGT	CCAGTATATG	CAATACACTT	4800
881 TGTATACAG	TCTTACT	TCTCTGTCAT	AAAAATGTGC	4880

4898

FIG. 1DE

10	20	30	40	50	60	70	80
HVMIAFL PTILNQLFRV	LTRATOEEVA VNVTTRVIIHV	VAQCHEEGLE SHLRSYVKYA	YKAEPYVASE YKTVHEELTK	80			
TILKPSA DFLTSNKLLR	YSWFFFDVLI KSMAQHlien	SKVILLRNQR FPASYHHAEE	TVVNMMLMPHI TOKFGDNPEA	160			
IANHSLAV FIXRCFTFMD	RGFVFQIQINN YISCFAPGDP	KTLFYKFEF LRVVCNHEHY	IPLNLPMPFG KGRIQRYQDL	240			
JYSLTDEF CRNHFLVGLL	LRVGTAQOE FREVRLIAIS	VLKNILLIKHS FDDRYASRSH	QARLATLYLP LPGLLIEENVQ	320			
JVRUVSPF PVNAGMTVKD	ESLALPAVNP LVTPOKGSTL	DNSLHKDLLG AISGLASPYT	TSTPNINSVR NADSRGSLIS	400			
SGNSLPER NSEKSNSLDK	HOQSSTLGNs VVRCDKLDQS	EIKSLLMCFL YILKSMSSDA	LFTYWNKAST SELMDFFTIS	480			
CLHQFOYM GKYIARNQE	GLGPTVHDRK SOTLPVSRNR	TGMMIHARLQQ LGSLDNSLTF	NHSYGHSDAD VLHOSLLEAN	560			
TEVCLTAL DTLSLFTLAF	KNQLLADHGH NPLMKVFDV	YLCFLQKHQS ETALIQNFTA	LRSLIYKPPS TFYEGRADMC	640			
LCYEILKC CNSKLSSIRT	EASQLLYFLM RNNFDYTGKK	SFVRTHLQVI ISVSQLIADV	VGIGETRPOQ SLSIINNCAN	720			
RLIKHTSF SSDVKDLTKR	IRTVLMATAQ MKEHENOPEM	LVDLQYSLAK SYASTPELRK	TWLDMSMARH VNGDLSEAA	800			
JVHVTALV AEYLTRKGVF	RGCTAFRVI TPNIDEEASM	MEDVGMQDVH FNEDVLMELL	EOCADGLWKA ERYELLADIY	880			
JIPPIYEKR RDFFEDEDGK	EYTYKEPLT PLSEISQRLL	KLYSDKFGSE NVKMIQDSGK	VNPKDLDISKY AYIQVTHVIP	960			
DEKELOER KTEFERSHNI	RRFMFEMPP QTGKRQGGVE	EQCKRKTILT AIHCFPYVKK	RIPVMYQHHT DLNPIEVAID	1040			
4SKIVAELR OLCSSAEVDM	IKLQLKLOGS VSVQVNAGPL	AYARAPLDDT NTKRYPDNKV	KLJKEVFRQF VEACGQALAV	1120			
ERLIKEDQL EYQEEMKANY	REMAKELSEI MHEQICPLEE	KTSVLPNSLH IFNAISGPT	STMVHGMTSS SSVV	1194			
10	20	30	40	50	60	70	80

FIG. 1DE (cont.)

	10	20	30	40
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG
2	GAATTGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA
3	ATGAAAAGCA	CCACCTGTTG	CTCACATCT	TCCATGTCAG
4	GTCGTTGAAA	CCCAGTTGG	CTACTCTGG	CTTCCCCCTCC
5	GGTCTCGGCG	AACCTCCCT	CGGGCTATCT	TGGCTACCAA
6	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAA	TTTCCACTCA
7	ATTTTTCCA	GTACTGTCAG	AAAACCGAA	CTGGAGGCCA
8	CATGGGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCCA
9	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT
10	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC
11	ACCAAATCCA	TGACCACGAT	TCTCAAGCT	TCTGCGGATT
12	CTTGTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA
13	CTGCATCTA	TCATCATGCA	GGGGAAACCG	TTGTAATAT
14	GAGGCATCTA	AGAACGCGAA	TCATAGCTT	GCTGCTCTCA
15	CAAGCAGATC	AAACRACTACA	TTAGCTGTT	TGCTCCCTGGA
16	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT
17	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA
18	GACAGCCCTC	CAGGAGTCC	GGGAGGTCCG	TCTGATGCC
19	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC
20	GTCCAGCGGA	TCATGTGAG	GGATGTGTC	CCCTTCCCTG
21	ACCAAGCTGTG	AATCCGTGG	TGACGCCGCA	GAAGGGAAAGC
22	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA
23	ATAAGCACAG	ATTCGGTAA	CAGCCTTCCA	GAAGGAAATA
24	CACATTGGGA	AATTCCGTTG	TTGCTGTTGA	TAACACTTGAC
25	TCTTAAAGAG	CATGTCGAT	GATGCTTGT	TTACATATTG
26	ATATCTGAAG	TCTGCTGCA	CCAGTTCCAG	TACATGGGGA
27	AGTTCATGAT	CGAAAGCTC	AGACATGCC	TGTTTCCCGT
28	GCAGECTGGA	TAACCTCTC	ACTTTAAC	ACAGCTATGG
29	GCCACCATG	CTACTGAGGT	TTGCTGACA	GCTCTGGACA
30	GGCGGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT
31	CGGTTTAAA	AAATGTCTC	ACTGCCCTAA	GGTCTTAAT
32	ATGTGTGCGG	CTCTGIGTTA	CGAGATTCTC	AAGTGTGTA
33	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTGGA
34	CTGTCAGCCA	GCTGATAGCA	GACGTTGTTG	GCATGGGGA
35	GCCAAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCT
36	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCA
37	ATGGEAGCAC	GCCCCAGCTC	AGGAAGACGT	GGCTGACAG
38	GCAGCAATGT	GCTATGTCCA	CGTAAACAGCC	CTAGTGGCAG
39	CGCCTTCAGG	GTCAATTACCC	CAAACATCGA	CGAGGAGGCC
40	ACGAGGATGT	GCTGATGGAG	CTCCCTGAGC	AGTGGCGAGA
41	ATGACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG
42	GGAAACCCAAA	CTCACACCGC	TGTGGAAAT	TTCTCAGAGA
43	TCATAATGAT	ACAGGATCT	GGCAAGGTCA	ACCCCTAACCGA
44	ATGCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA
45	TGAGATGCCA	TTTACGCGA	CCGGGAAGAG	GCAGGGGGGG
46	TACACTGCTT	CCCTTATGTG	AAAGAGCGCA	TCCCCTGTCAT
47	ATPGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC
48	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGGT	CAATGCTGGC
49	CAAAGCGATA	TCCGTACAAT	AAAGTGAAGC	TGCTTAAGGA
50	GGGGTAAACG	AACGTCTGAT	TAAGAGAAC	CAGCTCGAGT
51	GGAGCTTCT	GAATCATGC	ATGAGCAGAT	CTGCCCCCTG
52	TCAACGCCAT	CAGTGGGACT	CCAACAAAGCA	CAATGGTCTCA
53	ATGGCCCGTG	TGTGGGACT	TGCTTGTCA	TTTGCCTAACT
54	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAAG
55	AGAAGGTGCA	CATATTTTT	TAATCTCAC	TGGCAATATT
56	TCTTGAGCTG	GACTTAGATT	TTATCTCTC	TTGCAAGAGTA
57	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCCTG
58	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG
59	ATAGAGCAAG	ATAGTGTGAGC	TAATGAGCT	AGACACTCAA
60	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA
61	TGTGATAAAT	TGTGCTGGT	CCAGTATATG	CAATACACTT
62	TGTATAACAG	TCTTACT		

	50	60	70	80
1	GCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC
2	TTTATGATG	AGATTAAT	AGAGTTGCC	ACTCAGCTGC
3	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
4	TGAAAGACGG	AAGGGTGGT	ACAAGCGAGC	AGCACATCCC
5	GAGCTGGGA	TGGCAGGCA	TTATGGTCG	AAAATTAAT
6	TCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA
7	AGCCTTAGGA	AACGAACITG	TAAAGTACCT	TAAGAGTCG
8	CTATCCTAAA	CCAGCTGTC	CGAGTCCTCA	CCAGAGCCAC
9	CATGTGGTIG	CCCAGTGCC	TGAGGAAGGA	TTGGAGAGCC
10	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
11	TCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTT
12	GAGAACTCCA	AAGTTAAGT	GCTGCGAAC	CAGAGATTC
13	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
14	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTGTCTT
15	GACCCAAAGA	CCCTCTTGA	ATACAAGTTT	GAATTTCTCC
16	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA
17	GAARACCACT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
18	ATCAGTGTG	TCAAGAACCT	GCTGATAAAG	CATTCTTTG
19	CACCCCTCTAC	CTGCTCTGT	TTGGCTGCT	GATTGAAAAC
20	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
21	ACCCCTGGACA	ACAGCTGCA	CAAGGACCTG	CTGGGGGCCA
22	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC
23	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
24	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTG	TTCCCTCTACA
25	GAACRAAGGT	TCAACATCTG	AACTTATGGA	TTTTTTACA
26	ACCGATAACAT	AGCCAGGAAC	CAGGAGGGGT	TTGGACCCAT
27	AAACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
28	CCACTCGGAC	GCAGATGTC	TGCACCCAGTC	ATTACTTGA
29	CGCTTCTCT	ATTTACATTG	GCGTTTAAGA	ACCAAGCTCT
30	GATGTCACC	TGTTGTTTCT	TCAAAAACAT	CAGTCTGAAA
31	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
32	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT
33	AAGAAGTCCT	TTGTCGGAC	ACATTGCAA	GTCATCATAT
34	AACCAAGATTC	CAGCAGTCCC	TGTCACATCAT	CAACAACTGT
35	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGT
36	GAGATGCTGG	TGGACTCTCA	GTACAGCTG	GCCAAATCT
37	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCGAG
38	AATATCTCAC	ACGGAAAGGC	GTGTTAGAC	AAGGATGAC
39	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTA
40	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCCGAC
41	ATTTCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
42	CTCCTTAAAC	TGTACTCGGA	TAATTTGGT	TCTGAAAATG
43	TCTGGATTCT	AAGTATGAT	ACATCCAGGT	GACTCAGCTC
44	CAGAGTTTGA	GAGATCCCAC	AAACATCCGCC	GCTTCATGTT
45	GTGGAAAGAGC	AGTGCRAACG	GCGCACCCTC	CTGACAGCCA
46	GTACCAAGCAC	TGAAACCCAT	CGAGGTGGCC	3680
47	TGTGCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
48	CCACTAGCAT	ATGCGCGAGC	TTTCCTAGAT	GATACAAACA
49	AGTTTCAGG	CAATTGTTG	AAGCTTGCGG	TCAAGCTTA
50	ATCAGGAAGA	AAATGAAAGCC	AACTACAGGG	AAATGGCGAA
51	GAGGAGAAGA	CGAGGGCTT	ACCGAATTCC	CTTCACATCT
52	CGGGGATGACC	AGCTCGTCIT	'CGGTGTTGTC	ATTACATCTC
53	CAGGATGCTT	TCCAAGCCA	ATCACTGGG	4160
54	AACAACGTTA	TTTCTTAACA	GACTTTCTAT	AGGAGTTGTA
55	CAAAGTTTTC	ATTGTCCTT	AAACAAAGGTG	TTGGTAGACAC
56	GTGTTAGAAT	AGATGGCTA	CAGAAAAAAA	AGGTTCTGGG
57	GGGGACCTT	TGCCTCGACT	CGTGCCTGGAA	ATCIGATCGT
58	TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCAACAC
59	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TGTCATTA
60	CATTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTTAAT
61	TGTGATAAAT	TGTGCTGGT	CCAGTATATG	CAATACACTT
62	TGTATAACAG	TCTTACT		

FIG. 10F

10	20	30	40	50	60	70	80
EVNIAFL PTILNQLFRV	LTRATOEEVA VNVTIRVIIHV	YKAEPYVASE YKTVHEELTK	80				
TIKPSA DFLTSNLLR	YSWFFFVLI KSMAOHLIEN	SKVILLRNQR FPASYHAAE	160				
ANHSLAV FIKRCFTPMD	RGFVFKQINN YISCFAPGDP	TVVNMLMPHI TOXFGDNPEA	160				
YSLTDEF CRNHFLVGLL	LREVGTLAQE FREVRLIAIS	KLFEYKPEF LRVVCNHEHY	240				
VRDVSPF PVNAGMTVKD	ESLALPAVNP LVTPOKGSTL	QARIATLYLP LPGLLIENVQ	320				
IGNSLPER NSEKENSLOK	HQQSSTLGN S VRCDDKLDQS	DNSLHDOLLG AISGLASPYT	400				
LHQFQYM GKRYIARNOE	GLGPIVHDK SQTLFVSRNR	EIKSLLMCFL YILKMSDDA	480				
EVCLTAL DTLSLFTLAF	KNQLLAHDGH NPLMKKVFDV	LPTYWNIKAST SELMDFFTIS	480				
UCYEILKC CNSKLSSIRT	EASQLLYFLM RNNFDYTGKK	TGMMHARLQQ LGSLDNSTF	560				
RLIKHTSF SSDVADLTIR	IRTVLMMATAQ MKEHENDPEM	NHSYGHSDAD VLNQSLLEAN	560				
YHVTALV AEYLTRKGVF	ROGCTAFRVI TPNIDEEASM	YLCFLQKHQS ETALQWPTA	640				
IIPIYER RDFFEDEDGK	EYIYKEPLT PLSEISQRLL	SFVRTHILOVI ISVSQLLADV	720				
DEKELOER KTEFERSHNI	RRFMFEMPPT QTGKROQGGVE	LVDLQYSLAK SYASTPELRK	800				
ISKKVAELR QLCSSAEVDM	IKLOLQKLOGS VSVQVNAGPL	MEDVGMQDVH FNEQVILMELL	880				
IRLIKEDQL EYCEEMKANY	REMAKELSEI MHEQICPLEE	EQCADGLWKA ERYELIADTY	880				
		KLYSDKFGSE NVIMIQDSGK	960				
		VNPKDLDISKY AYIQVTHVIP	960				
		EQCKRRTILT AIHCFPYVKK RIPVMYQHHT	1040				
		DLNPIEVAID AYARAPLIDT	1120				
		NTKRYPONKV KLLKEVFRQP	1120				
		VEACGQALAV KTSVLPNSLH	1194				
10	20	30	40	50	60	70	80

FIG. 1DF (cont.)

	10	20	30	40		50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCCTG	CTTCCCCCTCC	TGAAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGCG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA	480
481	ATTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGGCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTG	CGAGTCCTCA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGC	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCT	TCTGCCGATT	TCCTCACCAG	CAACAAACTA	CTGAGGTA	CATGGTTTT	880
881	CTTTGATGTA	CTGATCAAT	CTATGGCTCA	GCATTGATA	GAGAACTCCA	AGTTAAGTT	GCTGCGAAAC	CAGAGATTT	960
961	CTGCATCCTA	TCATCATGCA	GGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACCGCGAA	TCATAGCTT	GCTGCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTGTCTT	1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTT	TGCTCTGGG	GACCCAAAGA	CCCTCTTGA	ATACAAGTT	GAATTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATT	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATGCC	ATCAGTGTG	TCAAGAACCT	GCTGATAAAAG	CATTCTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTG	TTGGCTG	GATTGAAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTTGCA	CCCTTCCCTG	TGAACGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAGC	ACCCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGGGCCA	1680
1681	TCTCCGGCAT	TGCTCTTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTGGGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCCGTGG	TTCGCTGTGA	AAACATTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTG	TTCCCTTACA	1920
1921	TCTTAAAGAG	CATGTCGAT	GATGTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCTGCA	CCAGTTCCAG	TACATGGGG	AGCGATAACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2080
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCCT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTG	TGCACCGATC	ATTACTTGAA	2240
2241	GCCAACATTG	CTACTGAGGT	TTGCTTGACA	GCTCTGGACA	CGCTTCTCT	ATTACATTG	GCGTTTAAGA	ACCAGCTCCT	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT	GATGCTTAC	TGTTTCT	TCAAAACAT	CAGTCTGAAA	2400
2401	CGGCTTAAA	AAATGTCTC	ACTGCCCTAA	GGTCTTAAAT	TTATAAGTT	CCCTCAACAT	TCTATGAGG	GAGAGCGGAC	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGGATTCTC	AAAGTGTGTA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCGACT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTGGA	AAGAAGTCCT	TTGTCGGAC	ACATTGCAA	GTCATCATAT	2640
2641	CTGTCAGCCA	GCTGATAGCA	GACGTGTTG	GCATTGGGG	AACCAGATTG	CAGCAGTCCC	TGTCATCAT	CAACAACGT	2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGCT	2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	GCCCAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTC	AAAATGGCGA	TCTCTCAGAG	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGTCAC	3040
3041	CGCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGG	GATGCAGGAT	GTCCATTCTA	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCCTGAGC	AGTGGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC	3200
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	ATTTCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTACAA	3280
3281	GGAAACCCAAA	CTCACACCCG	TGTCGGAAT	TTCTCAGAGA	CTCCCTTAAAC	TGTACTCGGA	TAATTTGGT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AGTATGCT	ACATCCAGGT	GACTCACGTC	3440
3441	ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACCGAGA	CCGGGAAGAG	GCAGGGGGGG	GTGGAAGAGC	AGTGC	GGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAACGCA	TCCCTGTCAT	GTACAGCAGAC	CACACTGACC	TGAACCCAT	CGAGGTGGCC	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCA	3760
3761	CAAACCTCAG	GGCAGCGTGA	GTGTTGAGGT	CAATGCTGGC	CCACTAGCAT	ATGCGCAGC	TTTCTTAGAT	GATACAAACA	3840
3841	CAAAGCGATA	TCCGTACAAT	AAAGTGAAGC	TGCTTAAGGA	AGTTTCAGG	CAATTGTTG	AAGCTTGCGG	TCAAGCCTTA	3920
3921	GCGGTAAACG	AACGTCGAT	TAAAGAACAC	CAGCTGAGT	ATCAGGAAGA	AAATGAAAGCC	AACTACAGGG	AAATGGCGAA	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCTC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCGTGTG	ATTACATCTC	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTC	TTTGCAAAC	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AAACACGTTA	TTTCTTAACA	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTT	TTAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTCGTT	AAACAAGGTG	TGGTAGACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCCTCC	TTGCAAGAGTA	GTGTTAGAAT	AGATGGCTA	CAGAAAAAAA	AGGTTCTGGG	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACGAC	TTGATGCC	GGGGACCTTT	TGCCTCGACT	CGTGCAGGAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG	TIGTATGACT	AGGATTGTTG	CTATTATCTC	ATTCAACAAAC	4640
4641	ATAGAGCAAG	AATAGTGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTA	CATTTTTAAT	ACTCACATGG	GCTTATGCT	TAAGTTAAT	4800
4801	TGTGATAAAT	TTGTGCTG	CCAGTATAIG	CAATACACTT	TAATGGTTTA	TTCTTGTCA	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAG	TCTTTACT							4898

FIG. 1D6

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL PTILNQLFRV	LTRATQEEVA VN VTRVIIHV	VAQCHEEGLE SHLRSYVKYA	YKAEPYVASE YKTVHEELTK	80			
81	SMTTILKPSA DFLTSNKLLR	YSWFFF DVLI KSMAQH LIEN	SKVKLLRNQR FPAS YHAAE	TVVNMLMPHI TQKPGDNPEA	160			
161	SKNAHSLAV FIKRCFTFMD	RGFVFKQINN YISCFAPGDP	KTLFEYKFEF LRVVCNHEHY	IPLNLPMPPFG KGRIQRYQDL	240			
241	QLDYSLTDEF CRNHFLVGLL	LREVGTALQE FREVRLIAIS	VLKNLLIKHS FDDRYASRSH	QARIATLYLP LPGLLIENVQ	320			
321	RINVRDVSPF PVNAGMTVKD	ESLALPAVNP LVTPQKGSTL	DNSLHKDLLG AISGIA SPYT	TSTPNINSVR NADSRGSLIS	400			
401	TDSGNSLPER NSEKSNSLDK	HQQSSTL GNS VVRCDKLDQS	EIKSLLMCFL YILKSM SDDA	LFTYWNKA ST SELMDFFTIS	480			
481	EVCLHQFQYM GKRYIARNQE	GLGPIVHD RK SQ TLPVSRNR	TGMMHARLQQ LGSLDNSLTF	NHSYGHSDAD VLHQSILEAN	560			
561	IATEVCLTAL DTLSLFTLAF	KNQLLADHGH NPLMKKVFDV	YLCFLQKHQS ETALKNVFTA	LRSLIYKFPS TFYEGRADMC	640			
641	AALCYEILKC CNSKLSSIRT	EASQLLYFLM RNNFDYTGKK	SFVRTHLQVI ISVSQLIADV	VGIGETRFQQ SLSIINNCAN	720			
721	SDRLIKHTSF SSDVKDLTKR	IRT VLMATAQ MKEHENDPEM	LVDLQYSLAK SYASTPELRK	TWLDMSMARIH VKNGDLSEAA	800			
801	MCYVHVTALV AEYLTRKGVP	RQGCTAFRVI TP NIDEEASM	MEDVGMQDVH FNEDVLMELL	EQCADGLWKA ERYELIADIY	880			
881	KLIPIPIYEKR RDFFEDEDGK	EYIYKEPKLT PLSEI SQRLL	KLYSDKFGSE NVKMIQDSGK	VNPKDLD SKY AYIQVTHVIP	960			
961	FFDEKELOER KTEFERSHNI	RRFMFEMPFT QTGKRQGGVE	EQCKRRTILT AIHCFPYVKK	RIPVMYQHHT DLNPIEVAID	1040			
1041	EMSKKVAELR QLCSSAEVDM	IKLQLKLQGS VSVQVNAGPL	AYARAFLDDT NTKRYPDNKV	KLLKEVFRQF VEACGQALAV	1120			
1121	NERLIKEDQL EYQEEMKANY	REMAKELSEI MHEQICPLEE	KTSVLPNSLH IFNAISGTPT	STMVHGMTSS SSVV	1194			
	10	20	30	40	50	60	70	80

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### FIG. 10G (cont.)

	10	20	30	40		50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCCC	GAGGTGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCCGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTGG	CTACTCCCTG	CTTCCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGCAGGCA	TTATGGTCCG	GAAATTAAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA	480
481	ATTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGGCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATGCC	TTCTTGCCCA	CTATCCTAA	CCAGCTGTC	CGAGTCCCTCA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGTTG	CCCAGTGCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAATCCA	TGACCACGGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTT	880
881	CTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA	GAGAACTCCA	AAGTTAAGT	GCTGCGAAC	CAGAGATTC	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACCGGAA	TCATAGCTT	GCTGTCCTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGCTT	1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTT	TGCTCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTTC	CGTTGAACCTT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTG	TCAAGAACCT	GCTGATAAAAG	CATTCTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTCTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTC	CCCTTCCCTG	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGGCGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTGGGGTAA	CAGCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCCGTGG	TTGCTGTGA	TAACATGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTG	TTCTCTTACA	1920
1921	TCTTAAAGAG	CATGTCGTAT	GATGTTTGT	TTACATATTG	GAACAAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCCTGCA	CCAGTTCCAG	TACATGGGG	AGCGATACT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2080
2081	AGTTCATGAT	CGAAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AAACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2161	GCAGCTGGA	TAACCTCTTC	ACTTTAACCC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTC	TGCACCAGTC	ATTACTGAA	2240
2241	GCCAACATTG	CTACTGAGGT	TTGCTGTGCA	GCTCTGGACA	CGCTTTCTCT	ATTACATTTG	GCGTTTAAGA	ACCAGCTCT	2320
2321	GGCGGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTT	GATGCTTACCC	TGTGTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2401	CGGCTTAAA	AAAATGCTTC	ACTGCTTAA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGGATTCTC	AAGTGTGTA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTGA	TTACACTGGA	AAGAAGTCCT	TTGTCCGGAC	ACATTGCAA	GTCATCATAT	2640
2641	CTGTCAAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGG	AACCAGATT	CAGCAGTCCC	TGTCCATCAT	CAACAACIGT	2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCT	CTGATGTGAA	GGACCTAAC	AAAAGGATAC	GCACGGTGT	2800
2801	AATGGCCACC	GCCCGAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	GCCCGAGGTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGTCAC	3040
3041	CGCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC	3200
3201	ATCTACAAAC	TTATCATCTCC	CATTATGAG	AAGCGGAGGG	ATTTCTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTACAA	3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAT	TTCTCAGAGA	CTCCCTTAAAC	TGTACTCGGA	TTAATTGAGT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCCTAACCGA	TCTGGATTCT	AAAGTATGCA	ACATCCAGGT	GACTCACGTC	3440
3441	ATCCCCCTCT	TTGACGAAAAA	AGAGTTGCAA	GAAAGGAAAAA	CAGAGTTTGA	GAGATCCCAC	AAACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACGCGAGA	CCGGGAAGAG	GCAGGGGGGG	GTGGAAGAGC	AGTGCACACG	GCGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCAT	GTACCCAGCAC	CACACTGACCC	TGAACCCCCAT	CGAGGTGGCC	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCTTC	GGCCGAGGTG	GACATGATCA	AACTGAGCT	3760
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAGGT	CAATGTCAGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATAACAAACA	3840
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAGGA	AGTTTTCAGG	CAATTGTTG	AAGCTTGCGG	TCAAGCCTTA	3920
3921	GCGGTAAACG	AACGTCTGAT	AAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	ATGAAAGGCC	AACTACAGGG	AAATGGCGAA	4000
4001	GGAGCTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCCT	ACCGAATTCC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTC	CGGGATGACC	AGCTCGTCCT	CGGTGCGTGTG	ATTACATCTC	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACCT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AAACACGTTA	TTTCTTAACA	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTT	TTAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGTCCT	AAACAAGGTG	TGGTAGACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCCTCC	TTGCGAGAGTA	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTG	GGGGACCTTT	TGCCTCGACT	CGTGCAGGAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG	TTGTATGACT	AGGAGTTGTG	CTATTATCTC	ATTCAACAAAC	4640
4641	ATAGAGCAAG	AAATAGTGGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTAA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTA	CATTTTAAT	ACTCACATGG	GCTTATGCA	TAAGTTTAAT	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCA	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAAG	TCTTTACT							4898
	10	20	30	40		50	60	70	80

FIG. 10H

	10	20	30	40	50	60	70	80
1	MEGHVIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK
81	SMTILKPSA	DFLTSNKLLR	YSWFFFVLI	KSMAQHlien	SKVILRNQR	FPASYHHAAE	TVVNMMPHI	TQKPGDNPEA
161	SKNAHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNs	VVRCDKLDQS	EIKSLLMCFL	YILKMSDDA	LFTYWNKAST	SELMDFFTIS
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDINSLT	NHSYGHSDAD	VLHQSLLEAN
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDMSMARH	VKNGDLSEAA
801	MCYVHVTALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELLIADIY
881	KLIPIYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRILL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDISKY	AYIQVTHVIP
961	FFDEKELEQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID
1041	EMSKVVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV
1121	NERLIKEDQ	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTP	STMVHGMTSS	SSVV
	10	20	30	40	50	60	70	80

0  
100  
200  
300  
400  
500  
600  
700  
800  
900

FIG. 10H (cont.)

Exon 1A (-182 to -102)

GCAGGGGAAAAACCTGGCCCCATGATTCACTTACTTCCCACCGGATCTCTCCCATGACACGTGAGGATTA  
TTACAATTAA -102

Exon 1B (-219 to -102)

TTATCCCTTACTTACTTGCAGTGGAGTCGGTAGATGGGAGTGGAGAAGAGAACCTTAGAATCATTGTTAGTCTTCAT  
CTTCACAGCTCAGGCTGAAGGCCTTCCTGCTGAGA -102

Exon 1C (-143 to -102)

CGGGCAGAGCGTGTCTGAGGTGGTGCAGCGGCTCCGTGCTCCT -102

Exon2 and the rest of human CLASP2 cDNA

-101 -79  
GGCAAAGCCAAAGCTAATTGAGC

-78 -1  
AAGCTAATTGAGCCACTCGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGTTACGGGAG

1/1 31/11  
ATG CTG CTC TTC CCT TAC GAT GAC TTT CAG ACG GCC ATC CTG AGA CGA CAG GGT CGA TAC  
Met leu leu phe pro tyr asp asp phe gln thr ala ile leu arg arg gln gly arg tyr

61/21 91/31  
ATA TGC TCA ACA GTG CCT GCG AAG GCG GAA GAG GAA GCA CAG AGC TTG TTT GTT ACA GAG  
ile cys ser thr val pro ala lys ala glu glu glu ala gln ser leu phe val thr glu

121/41 151/51  
TGC ATC AAA ACC TAT AAC TCT GAC TGG CAT CTT GTG AAC TAT AAA TAT GAA GAT TAC TCA  
cys ile lys thr tyr asn ser asp trp his leu val asn tyr lys tyr glu asp tyr ser

181/61 211/71  
GGA GAG TTT CGA CAG CTT CCG AAC AAA GTG GTC AAG TTG GAT AAA CTT CCA GTT CAT GTC  
gly glu phe arg gln leu pro asn lys val val lys leu asp lys leu pro val his val

241/81 271/91  
TAT GAA GTT GAC GAG GAG GTC GAC AAA GAT GAG GAT GCT GCC TCC CTT GGT TCC CAG AAG  
tyr glu val asp glu glu val asp lys asp glu asp ala ala ser leu gly ser gln lys

301/101 331/111  
GGT GGG ATC ACC AAG CAT GGC TGG CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC AGC GTG  
gly gly ile thr lys his gly trp leu tyr lys gly asn met asn ser ala ile ser val

361/121 391/131  
ACC ATG AGG TCA TTT AAG AGA CGA TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA TCC TAT  
thr met arg ser phe lys arg arg phe phe his leu ile gln leu gly asp gly ser tyr

421/141 451/151  
AAT TTG AAT TTT TAT AAA GAT GAA AAG ATC TCC AAA GAA CCA AAA GGA TCA ATA TTT CTG  
asn leu asn phe tyr lys asp glu lys ile ser lys glu pro lys gly ser ile phe leu

481/161 511/171  
GAT TCC TGT ATG GGT GTC GTT CAG AAC AAC AAA GTC AGG CGT TTT GCT TTT GAG CTC AAG  
asp ser cys met gly val val gln asn asn lys val arg arg phe ala phe glu leu lys

541/181	571/191
ATG CAG GAC AAA AGT AGT TAT CTC TTG GCA GCA GAC AGT GAA GTG GAA ATG GAA GAA TGG	met gln asp lys ser ser tyr leu leu ala ala asp ser glu val glu met glu glu trp
601/201	631/211
ATC ACA ATT CTA AAT AAG ATC CTC CAG CTC AAC TTT GAA GCT GCA ATG CAA GAA AAG CGA	ile thr ile leu asn lys ile leu gln leu asn phe glu ala ala met gln glu lys arg
661/221	691/231
AAT GGC GAC TCT CAC GAA GAT GAT GAA CAA AGC AAA TTG GAA GGT TCT GGT TCC GGT TTA	asn gly asp ser his glu asp asp glu gln ser lys leu glu gly ser gly ser gly leu
721/241	751/251
GAT AGC TAC CTG CCG GAA CTT GCC AAG AGT GCA AGA GAA GCA GAA ATC AAA CTA AAA AGT	asp ser tyr leu pro glu leu ala lys ser ala arg glu ala glu ile lys leu lys ser
781/261	811/271
GAA AGC AGA GTC AAA CTT TTT TAT TTG GAC CCA GAT GCC CAG AAG CTT GAC TTC TCA TCA	glu ser arg val lys leu phe tyr leu asp pro asp ala gln lys leu asp phe ser ser
841/281	871/291
GCT GAG CCA GAA GTG AAG TCA TTT GAA GAG AAG TTT GGA AAA AGG ATC CTT GTC AAG TGC	ala glu pro glu val lys ser phe glu glu lys phe gly lys arg ile leu val lys cys
901/301	931/311
AAT GAT TTA TCT TTC AAT TTG CAA TGC TGT GTT GCC GAA AAT GAA GAA GGA CCC ACT ACA	asn asp leu ser phe asn leu gln cys cys val ala glu asn glu glu gly pro thr thr
961/321	991/331
AAT GTT GAA CCT TTC TTT GTT ACT CTA TCC CTG TTT GAC ATA AAA TAC AAC CGG AAG ATT	asn val glu pro phe phe val thr leu ser leu phe asp ile lys tyr asn arg lys ile
1021/341	1051/351
TCT GCC GAT TTC CAC GTA GAC CTG AAC CAT TTC TCA GTG AGG CAA ATG CTC GCC ACC ACG	ser ala asp phe his val asp leu asn his phe ser val arg gln met leu ala thr thr
1081/361	1111/371
TCC CCG GCG CTG ATG AAT GGC AGT GGG CAG AGC CCA TCT GTC CTC AAG GGC ATC CTT CAT	ser pro ala leu met asn gly ser gly gln ser pro ser val leu lys gly ile leu his
1141/381	1171/391
GAA GCC GCC ATG CAG TAT CCG AAG CAG GGA ATA TTT TCA GTC ACT TGT CCT CAT CCA GAT	glu ala ala met gln tyr pro lys gln gly ile phe ser val thr cys pro his pro asp
1201/401	1231/411
ATA TTT CTT GTG GCC AGA ATT GAA AAA GTC CTT CAG GGG AGC ATC ACA CAT TGC GCT GAG	ile phe leu val ala arg ile glu lys val leu gln gly ser ile thr his cys ala glu
1261/421	1291/431
CCA TAT ATG AAA AGT TCA GAC TCT TCT AAG GTG GCC CAG AAG GTG CTG AAG AAT GCC AAG	pro tyr met lys ser ser asp ser ser lys val ala gln lys val leu lys asn ala lys
1321/441	1351/451
CAG GCA TGC CAA AGA CTA GGA CAG TAT AGA ATG CCA TTT GCT TGG GCA GCA AGG ACA TTG	gln ala cys gln arg leu gly gln tyr arg met pro phe ala trp ala ala arg thr leu

1381/461	1411/471
TTT AAG GAT GCA TCT GGA AAT CTT GAC AAA AAT GCC AGA TTT TCT GCC ATC TAC AGG CAA	phe lys asp ala ser gly asn leu asp lys asn ala arg phe ser ala ile tyr arg gln
1441/481	1471/491
GAC AGC AAT AAG CTA TCC AAT GAT GAC ATG CTC AAG TTA CTT GCA GAC TTT CGG AAA CCT	asp ser asn lys leu ser asn asp asp met leu lys leu leu ala asp phe arg lys pro
1501/501	1531/511
GAG AAG ATG GCT AAG CTC CCA GTG ATT TTA GGC AAT CTA GAC ATT ACA ATT GAT AAT GTT	glu lys met ala lys leu pro val ile leu gly asn leu asp ile thr ile asp asn val
1561/521	1591/531
TCC TCA GAC TTC CCT AAT TAT GTT AAT TCA TCA TAC ATT CCC ACA AAA CAA TTT GAA ACC	ser ser asp phe pro asn tyr val asn ser ser tyr ile pro thr lys gln phe glu thr
1621/541	1651/551
TGC AGT AAA ACT CCC ATC ACG TTT GAA GTG GAG GAA TTT GTG CCC TGC ATA CCA AAA CAC	cys ser lys thr pro ile thr phe glu val glu glu phe val pro cys ile pro lys his
1681/561	1711/571
ACT CAG CCT TAC ACC ATC TAC ACC AAT CAC CTT TAC GTT TAT CCT AAG TAC TTG AAA TAC	thr gln pro tyr thr ile tyr thr asn his leu tyr val tyr pro lys tyr leu lys tyr
1741/581	1771/591
GAC AGT CAG AAG TCT TTT GCC AAG GCT AGA AAT ATT GCG ATT TGC ATT GAA TTC AAA GAT	asp ser gln lys ser phe ala lys ala arg asn ile ala ile cys ile glu phe lys asp
1801/601	1831/611
TCA GAT GAG GAA GAC TCT CAG CCC CTT AAG TGC ATT TAT GGC AGA CCT GGT GGG CCA GTT	ser asp glu glu asp ser gln pro leu lys cys ile tyr gly arg pro gly gly pro val
1861/621	1891/631
TTC ACA AGA AGC GCC TTT GCT GCA GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT	phe thr arg ser ala phe ala ala val leu his his his gln asn pro glu phe tyr asp
1921/641	1951/651
GAG ATT AAA ATA GAG TTG CCC ACT CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC	glu ile lys ile glu leu pro thr gln leu his glu lys his his leu leu leu thr phe
1981/661	2011/671
TTC CAT GTC AGC TGT GAC AAC TCA AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA	phe his val ser cys asp asn ser ser lys gly ser thr lys lys arg asp val val glu
2041/681	2071/691
ACC CAA GTT GGC TAC TCC TGG CTT CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG	thr gln val gly tyr ser trp leu pro leu leu lys asp gly arg val val thr ser glu
2101/701	2131/711
CAG CAC ATC CCG GTC TCG GCG TAC CTT CCT TCG GGC CAT CTT GGC TAC CAA GAG CTT GGG	gln his ile pro val ser ala tyr leu pro ser gly his leu gly tyr gln glu leu gly
2161/721	2191/731
ATG GGC AGG CAT TAT GGT CCG GAA ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA	met gly arg his tyr gly pro glu ile lys trp val asp gly gly lys pro leu leu lys

2221/741	2251/751
ATT TCC ACT CAT CTG GTT TCT ACA GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC	ile ser thr his leu val ser thr val tyr thr gln asp gln his leu his asn phe phe
2281/761	2311/771
CAG TAC TGT CAG AAA ACC GAA TCT GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC	gln tyr cys gln lys thr glu ser gly ala gln ala leu gly asn glu leu val lys tyr
2341/781	2371/791
CTT AAG AGT CTG CAT GCG ATG GAA GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA	leu lys ser leu his ala met glu gly his val met ile ala phe leu pro thr ile leu
2401/801	2431/811
AAC CAG CTG TTC CGA GTC CTC ACC AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT	asn gln leu phe arg val leu thr arg ala thr gln glu glu val ala val asn val thr
2461/821	2491/831
CGG GTC ATT ATT CAT GTG GTT GCC CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG	arg val ile ile his val val ala gln cys his glu glu gly leu glu ser his leu arg
2521/841	2551/851
TCA TAT GTT AAG TAC GCG TAT AAG GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG	ser tyr val lys tyr ala tyr lys ala glu pro tyr val ala ser glu tyr lys thr val
2581/861	2611/871
CAT GAA GAA CTG ACC AAA TCC ATG ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC	his glu glu leu thr lys ser met thr thr ile leu lys pro ser ala asp phe leu thr
2641/881	2671/891
AGC AAC AAA CTA CTG AGG TAC TCA TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT	ser asn lys leu leu arg tyr ser trp phe phe asp val leu ile lys ser met ala
2701/901	2731/911
CAG CAT TTG ATA GAG AAC TCC AAA GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC	gln his leu ile glu asn ser lys val lys leu leu arg asn gln arg phe pro ala ser
2761/921	2791/931
TAT CAT CAT GCA GCG GAA ACC GTT GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT	tyr his his ala ala glu thr val val asn met leu met pro his ile thr gln lys phe
2821/941	2851/951
GGA GAT AAT CCA GAG GCA TCT AAG AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA	gly asp asn pro glu ala ser lys asn ala asn his ser leu ala val phe ile lys arg
2881/961	2911/971
TGT TTC ACC TTC ATG GAC AGG GGC TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT	cys phe thr phe met asp arg gly phe val phe lys gln ile asn asn tyr ile ser cys
2941/981	2971/991
TTT GCT CCT GGA GAC CCA AAG ACC CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG	phe ala pro gly asp pro lys thr leu phe glu tyr lys phe glu phe leu arg val val
3001/1001	3031/1011
TGC AAC CAT GAA CAT TAT ATT CCG TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT	cys asn his glu his tyr ile pro leu asn leu pro met pro phe gly lys gly arg ile

3061/1021	3091/1031
CAA AGA TAC CAA GAC CTC CAG CTT GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC	gln arg tyr gln asp leu gln leu asp tyr ser leu thr asp glu phe cys arg asn his
3121/1041	3151/1051
TTC TTG GTG GGA CTG TTA CTG AGG GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC	phe leu val gly leu leu leu arg glu val gly thr ala leu gln glu phe arg glu val
3181/1061	3211/1071
CGT CTG ATC GCC ATC AGT GTG CTC AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA	arg leu ile ala ile ser val leu lys asn leu leu ile lys his ser phe asp asp arg
3241/1081	3271/1091
TAT GCT TCA AGG AGC CAT CAG GCA AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG	tyr ala ser arg ser his gln ala arg ile ala thr leu tyr leu pro leu phe gly leu
3301/1101	3331/1111
CTG ATT GAA AAC GTC CAG CGG ATC AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG	leu ile glu asn val gln arg ile asn val arg asp val ser pro phe pro val asn ala
3361/1121	3391/1131
GGC ATG ACC GTG AAG GAT GAA TCC CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG	gly met thr val lys asp glu ser leu ala leu pro ala val asn pro leu val thr pro
3421/1141	3451/1151
CAG AAG GGA AGC ACC CTG GAC AAC AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC	gln lys gly ser thr leu asp asn ser leu his lys asp leu leu gly ala ile ser gly
3481/1161	3511/1171
ATT GCT TCT CCA TAT ACA ACC TCA ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG	ile ala ser pro tyr thr ser thr pro asn ile asn ser val arg asn ala asp ser
3541/1181	3571/1191
AGA GGA TCT CTC ATA AGC ACA GAT TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG	arg gly ser leu ile ser thr asp ser gly asn ser leu pro glu arg asn ser glu lys
3601/1201	3631/1211
AGC AAT TCC CTG GAT AAG CAC CAA CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT	ser asn ser leu asp lys his gln gln ser ser thr leu gly asn ser val val arg cys
3661/1221	3691/1231
GAT AAA CTT GAC CAG TCT GAG ATT AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG	asp lys leu asp gln ser glu ile lys ser leu leu met cys phe leu tyr ile leu lys
3721/1241	3751/1251
AGC ATG TCT GAT GAT GCT TTG TTT ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG	ser met ser asp asp ala leu phe thr tyr trp asn lys ala ser thr ser glu leu met
3781/1261	3811/1271
GAT TTT TTT ACA ATA TCT GAA GTC TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC	asp phe phe thr ile ser glu val cys leu his gln phe gln tyr met gly lys arg tyr
3841/1281	3871/1291
ATA GCC AGG AAC CAG GAG GGG TTG GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG	ile ala arg asn gln glu gly leu gly pro ile val his asp arg lys ser gln thr leu

3901/1301	3931/1311
CCT GTT TCC CGT AAC AGA ACA GGA ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG	pro val ser arg asn arg thr gly met met his ala arg leu gln gln leu gly ser leu
3961/1321	3991/1331
GAT AAC TCT CTC ACT TTT AAC CAC AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG	asp asn ser leu thr phe asn his ser tyr gly his ser asp ala asp val leu his gln
4021/1341	4051/1351
TCA TTA CTT GAA GCC AAC ATT GCT ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT	ser leu leu glu ala asn ile ala thr glu val cys leu thr ala leu asp thr leu ser
4081/1361	4111/1371
CTA TTT ACA TTG GCG TTT AAG AAC CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG	leu phe thr leu ala phe lys asn gln leu leu ala asp his gly his asn pro leu met
4141/1381	4171/1391
AAA AAA GTT TTT GAT GTC TAC CTG TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA	lys lys val phe asp val tyr leu cys phe leu gln lys his gln ser glu thr ala leu
4201/1401	4231/1411
AAA AAT GTC TTC ACT GCC TTA AGG TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA	lys asn val phe thr ala leu arg ser leu ile tyr lys phe pro ser thr phe tyr glu
4261/1421	4291/1431
GGG AGA GCG GAC ATG TGT GCG GCT CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG	gly arg ala asp met cys ala ala leu cys tyr glu ile leu lys cys cys asn ser lys
4321/1441	4351/1451
CTG AGC TCC ATC AGG ACG GAG GCC TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT	leu ser ser ile arg thr glu ala ser gln leu leu tyr phe leu met arg asn asn phe
4381/1461	4411/1471
GAT TAC ACT GGA AAG AAG TCC TTT GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC	asp tyr thr gly lys lys ser phe val arg thr his leu gln val ile ile ser val ser
4441/1481	4471/1491
CAG CTG ATA GCA GAC GTT GTT GGC ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC	gln leu ile ala asp val val gly ile gly glu thr arg phe gln gln ser leu ser ile
4501/1501	4531/1511
ATC AAC AAC TGT GCC AAC AGT GAC CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG	ile asn asn cys ala asn ser asp arg leu ile lys his thr ser phe ser ser asp val
4561/1521	4591/1531
AAG GAC TTA ACC AAA AGG ATA CGC ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT	lys asp leu thr lys arg ile arg thr val leu met ala thr ala gln met lys glu his
4621/1541	4651/1551
GAG AAC GAC CCA GAG ATG CTG GTG GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC	glu asn asp pro glu met leu val asp leu gln tyr ser leu ala lys ser tyr ala ser
4681/1561	4711/1571
ACG CCC GAG CTC AGG AAG ACG TGG CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC	thr pro glu leu arg lys thr trp leu asp ser met ala arg ile his val lys asn gly

4741/1581	4771/1591
GAT CTC TCA GAG GCA GCA ATG TGC TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC	asp leu ser glu ala ala met cys tyr val his val thr ala leu val ala glu tyr leu
4801/1601	4831/1611
ACA CGG AAA GGC GTG TTT AGA CAA GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC	thr arg lys gly val phe arg gln gly cys thr ala phe arg val ile thr pro asn ile
4861/1621	4891/1631
GAC GAG GAG GCC TCC ATG ATG GAA GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT	asp glu glu ala ser met met glu asp val gly met gln asp val his phe asn glu asp
4921/1641	4951/1651
GTG CTG ATG GAG CTC CTT GAG CAG TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG	val leu met glu leu leu glu gln cys ala asp gly leu trp lys ala glu arg tyr glu
4981/1661	5011/1671
CTC ATC GCC GAC ATC TAC AAA CTT ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT	leu ile ala asp ile tyr lys leu ile ile pro ile tyr glu lys arg arg asp phe phe
5041/1681	5071/1691
GAA GAT GAA GAT GGA AAG GAG TAT ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA	glu asp glu asp gly lys glu tyr ile tyr lys glu pro lys leu thr pro leu ser glu
5101/1701	5131/1711
ATT TCT CAG AGA CTC CTT AAA CTG TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG	ile ser gln arg leu leu lys leu tyr ser asp lys phe gly ser glu asn val lys met
5161/1721	5191/1731
ATA CAG GAT TCT GGC AAG GTC AAC CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG	ile gln asp ser gly lys val asn pro lys asp leu asp ser lys tyr ala tyr ile gln
5221/1741	5251/1751
GTG ACT CAC GTC ATC CCC TTC TTT GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT	val thr his val ile pro phe phe asp glu lys glu leu gln glu arg lys thr glu phe
5281/1761	5311/1771
GAG AGA TCC CAC AAC ATC CGC CGC TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG	glu arg ser his asn ile arg arg phe met phe glu met pro phe thr gln thr gly lys
5341/1781	5371/1791
AGG CAG GGC GGG GTG GAA GAG CAG TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC	arg gln gly gly val glu glu gln cys lys arg arg thr ile leu thr ala ile his cys
5401/1801	5431/1811
TTC CCT TAT GTG AAG AAG CGC ATC CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC	phe pro tyr val lys lys arg ile pro val met tyr gln his his thr asp leu asn pro
5461/1821	5491/1831
ATC GAG GTG GCC ATT GAC GAG ATG AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC	ile glu val ala ile asp glu met ser lys lys val ala glu leu arg gln leu cys ser
5521/1841	5551/1851
TCG GCC GAG GTG GAC ATG ATC AAA CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG	ser ala glu val asp met ile lys leu gln leu lys leu gln gly ser val ser val gln

5581/1861	5611/1871
GTC AAT GCT GGC CCA CTA GCA TAT GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA	val asn ala gly pro leu ala tyr ala arg ala phe leu asp asp thr asn thr lys arg
5641/1881	5671/1891
TAT CCT GAC AAT AAA GTG AAG CTG CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC	tyr pro asp asn lys val lys leu leu lys glu val phe arg gln phe val glu ala cys
5701/1901	5731/1911
GGT CAA GCC TTA GCG GTA AAC GAA CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA	gly gln ala leu ala val asn glu arg leu ile lys glu asp gln leu glu tyr gln glu
5761/1921	5791/1931
GAA ATG AAA GCC AAC TAC AGG GAA ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG	glu met lys ala asn tyr arg glu met ala lys glu leu ser glu ile met his glu gln
5821/1941	5851/1951
ATC TGC CCC CTG GAG GAG AAG ACG AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC	ile cys pro leu glu glu lys thr ser val leu pro asn ser leu his ile phe asn ala
5881/1961	5911/1971
ATC AGT GGG ACT CCA ACA AGC ACA ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG	ile ser gly thr pro thr ser thr met val his gly met thr ser ser ser val val
5941/1981	5971
TGA TTA CAT CTC ATG GCC CGT GTG TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC	...
6001	6031
TTT CCA AAG CCA ATC ACT GGG GAG ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA	...
6061	6091
AAG GAA ATA AAG AAC AAC GTT ATT TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG	...
6121	6151
CAC ATA TTT TTT TAA ATC TCA CTG GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG	...
6181	6211
TGT GGT AGA CAC TCT TGA GCT GGA CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA	...
6241	6271
ATA GAT GGC CTA CAG AAA AAA AAG GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA	...
6301	6331
CAT TGA TGC CTG GGG GAC CTT TTG CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG	...
6361	6391
TAC AGA ACT TAC TAG TTT TGT CTA GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC	...
6421	6451
TCA TTC AAC AAC ATA GAG CAA GAA TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG	...
6481	6511
CTA CTG GCT TCA AGT CAG AAC TTT GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT	...
6541	6571
ATT ACA TTT CTA CAT TTT TAA TAC TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA	...
6601	6631
ATT TGT GCT GGT CCA GTA TAT GCA ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT	...
6661	
GCA ATA TGG AGA TGT ATA CAA GTC TTT ACT	

**A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-2 cDNA isoforms**

Isoform	Difference	Nucleotide(s)	Consequence
1	polymorphism	862	A to G change; mis-sense mutation
2	polymorphism		A to C change; mis-sense mutation changing codon from histidine to proline
3	polymorphism	2210	A to G change; mis-sense mutation changing codon from asparagine to glutamic acid
4	polymorphism	2225	C to T change; mis-sense mutation changing codon from histidine to tyrosine

**B. Alternative splices**

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	209-291	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-2 isoforms

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

### human CLASP-2

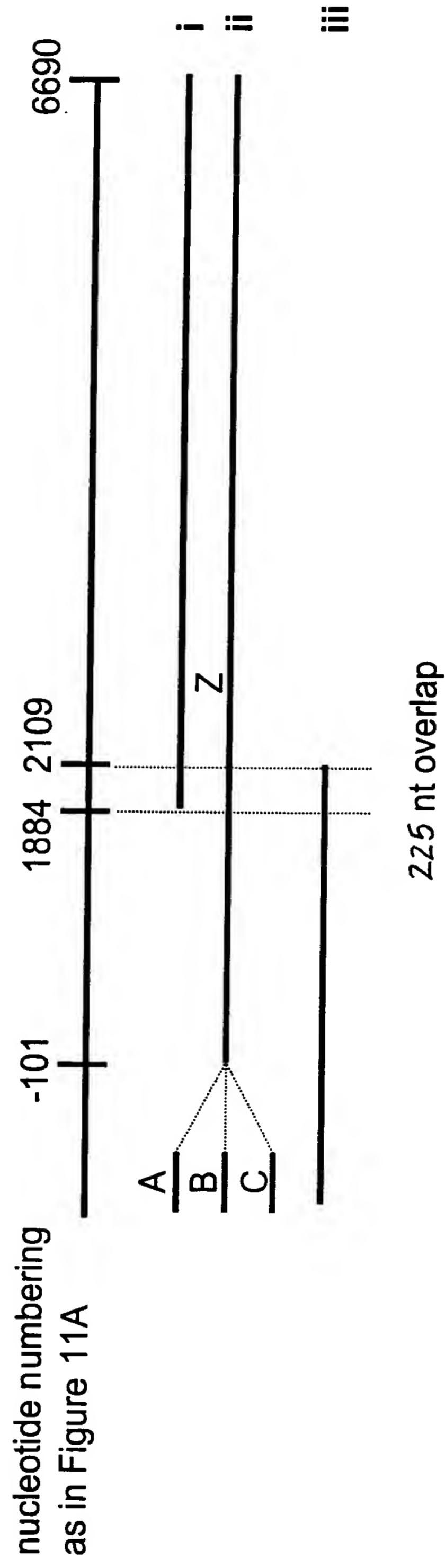


FIG. 11C

## 1st exon (nucleotides 335 to 445)

TGTCTTGCTTATCTTTGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACT  
CGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGT  
TTACGGGAGATGCTGCTTCCCTACGATGACTTCAGGTAAGTAACGTTAT  
GTTTCTATCCGTAGAACCAACG

## 2nd exon (nucleotides 7101-7190)

TTACCCAAGGCTTCCCTGTTTGTTCAGACGGCCATCCTGAGACGA  
CAGGGTCGATACATATGCTAACACAGTGCCTGCGAAGGCGGAAGAGGAAGCA  
CAGAGCTTGTGTTACAGAGGTAAGGCTTTCCCTGCATTAATTACATT  
GAAGTCATTCCCCTAACTGCCTCC

## 3rd exon (nucleotides 11439 to 11521)

TTTTCTATTTAAAATCCCCCTCAATAGTCATCAAAACCTATAACTCTGAC  
TGGCATCTTGTGAACTATAAATATGAAGATTACTCAGGAGAGTTCGACAGC  
TTCCGAAGTGAGTAAGCTATATTACACATAGGGAAAAGTCTT

## 4th exon (nucleotides 13987 to 14056)

CTAAAACAAATTCTTGTGTTTATAGCAAAGTGGTCAAGTTGGATAAA  
CTTCCAGTTCATGTCTATGAAGTTGACGAGGAGGTGACAAAGATGAGGTGG  
GATAACCTGCTGCTGTTCTCTTTCACTCTAGATTAA

## 5th exon (nucleotides 15212 to 15307)

GGAGGTTGACTGCTGGTTTTCCTCTCTCCTAGGATGCTGCCTCCCTGGTT  
CCCAGAAGGGTGGGATCACCAAGCATGGCTGGCTGTACAAAGGCAACATGA  
ACAGTGCCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTGCCCTC  
CCCTCTCACAAAGCCCTTC

## 6th exon (nucleotides 16269 to 16404)

TGAAAGAAATAGCTGTGTATATTTCTCTCAGTCATTAAAGAGACGATT  
TCCACCTGATTCAACTGGCGATGGATCCTATAATTGAATTAAAGAT  
GAAAAGATCTCCAAAGAACCAAAAGGATCAATATTCTGGATTCTGTATGG  
GTGTCGTTCAAGTAAATATGAAAAGAGTTTACCAATTATGTTCTTA

## 7th exon (nucleotides 19459 to 19633)

AAGTATGTCTGTTATCCTTTTCATTCAGAACAAACAAAGTCAGGCGTTT  
GCTTTGAGCTCAAGATGCAGGACAAAAGTAGTTATCTCTGGCAGCAGACA  
GTGAAGTGGAAATGGAAGAATGGATCACAATTCTAAATAAGATCCTCCAGCT  
CAACTTGAAGCTGCAATGCAAGAAAAGCGAAATGGCGACTCTCACGAAGGT  
AGATAGGCTTGGCTCCCCAGGCACATACACACTCT

## 8th exon (nucleotides 20567 to 20634)

ATTACAAGTGATTCCGATAATCTGTTTGCCTTTAGATGATGAACAAAGCA  
AATTGGAAGGTTCTGGTCCGGTTAGATAGCTACCTGCCGGAACTGCCAAG  
GTAACATCGTCTTATATCTTCTGCTCTCGTTGAATGC

9th exon (nucleotides 30257 to 30331)

GATTGTGTTAAATGTAATTTCATGTATCTTGTATCAGAGTGCAAGAGAAGC  
AGAAATCAAACAAAAAGTGAAGCAGAGTCAAACTTTTTATTGGACCCA  
GATGCCAGGTAAGAACTATCTAAATGTTAATATTAAAACCAAAT

10th exon (nucleotides 31851 to 31991)

CATAACTTATTATGTTACATTTCCTTTAAAGAACGCTGACTTCTCATCA  
GCTGAGCCAGAAGTGAAGTCATTGAAGAGAAGTTGGAAAAAGGATCCTTG  
TCAAGTGCAATGATTATCTTCAATTGCAATGCTGTGTTGCCGAAAATGAA  
GAAGGACCCACTACAAATGTAATTTCATTAAAAAATAAACATTAAAAAA  
AAAATAGGCAG

11th exon (nucleotides 32472 to 32675)

CCATGGTATCATTGGATTGTTGTTGTTCAAGGTTGAACCTTCTTGTAA  
CTCTATCCCTGTTGACATAAAATACAACCGGAAGATTCTGCCGATTCCAC  
GTAGACCTGAACCATTCTCAGTGAGGCAAATGCTGCCACCACGTCCCCGG  
CGCTGATGAATGGCAGTGGCAGAGCCCATCTGCCTCAAGGGCATCCTCA  
TGAAGCCGCCATGCAGTATCCGAAGCAGGTGGGGAGTATGAGCCCAGCATT  
CCACTACTCAGACTCACTTGCATGC

12th exon (nucleotides 33063 to 33185)

GAATTCTGCTTACTGAAGAAAATTGTTGCCTCCTAGGAAATTTTCAAGTCA  
CTTGTCCCTCATCCAGATATATTCTTGTGCCAGAATTGAAAAAGTCCTTCAG  
GGGAGCATCACACATTGCGCTGAGCCATATATGAAAAGTCAGACTCTTCTA  
AGGTATGAATGGCTTTACGCTTGGGTGGTAAAAAGCAATCTGAA

13th exon (nucleotides 36702 to 36784)

CAGTATCTCATAGCTTATTCTCATGTCTCAAGGTGGCCCAGAACAGGTGCTGA  
AGAATGCCAACGCAGGCATGCCAAAGACTAGGACAGTATAGAACGCCATTG  
TTGGGCAGCAAGGTAGGAACACACCTTTATACCTTAAATCGATATAGATA  
GGTGCATGG

14th partial exon (nucleotides 37353 to 37475)

GAAACCCAGTTAGAAATGTTGCTTGCCTTCAGGACATTGTTAAGGATG  
CATCTGGAAATCTTGACAAAAATGCCAGATTCTGCCATCTACAGGCAAGA  
CAGCAATAAGCTATCCAATGATGACATGCTCAAGTTACTGCAGACTTCGG  
AA

1 TACCAAGGGCAACTCTGGCACACCCCTAAAGTCTGGAAAGGGGACATAGCTAGTCAGGGATGACCCGAGAAATGACTGGAAGCTCCACCAAGAA  
93 TGCAGAGCTCCTTGTGCTTAAATAACTGAACAAGCATCACTCTGTGAGCAGGACACCACCCAGCATTGTCCTTGGAAACAACT  
185 CTTATTCTGTTCTTGTGATACCAAAACTAGCATACTCTAATTGTAGAAAATACAAACATAGAGTACAACATACTAAGTTCTTATCTT  
277 AAGAAATGGCATTGTGATGAGAATGTCTGCTTATCTTCGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACTCGACTATGAAATG  
369 TCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGTTACGGGAGATGCTGCTTCCCTACGATGACTTCAGGTAAGTAACGTTATG  
461 TTTCTATCCGTAGAACACACGTGTTGATCTAACAGCAGTATTTCTATGTATTGATTGTTGGTAGTTAATTATTATTATT  
553 ATTTTTGAGACACAGCTTGCTCTGTCACGCAGGCTTGAGTGCAGTGGTGCCTACGGCAACCTCCGCCTGGTTCA  
645 AGCATTCTCCTGCCCTCAGCCTCTCAAGTAACGGGATTACAGGCGTGTGCCACCATGCCTGGCTAATTGTCCTTGTATTAGAGACAGG  
737 GTTTGCCACGGTGGCCAGGGTCGCCCCAAACTCCTGCCCTAACGTGATCTATGCCTTGGCTCTCAAAATGTTGGGATTATAGGCATGA  
829 GCCACTGTGCCCGGCCCTAATTGGTTAAAAGATGAAAATAAGATGTTATTAAAGAAAGAAAAGTTATTATATTCTTCAAGCATCC  
921 TTCATGAGTTGATAATTAAAGGTATTATTTGCATATTAAAGTATGCCAAATGTGTGTGTGTGTGTGTGTGT  
1013 GTGTATCTTGAATAAAAGTGTACTCTGTCTGGCTGATTTAGTGGGACAAGTGCCTTCTGTCTTGGAGATTGTTGATTAGAT  
1105 TTTTGGCCAAGTACCTAGAACCTTAATGATGGCTTGGCTGGGAGCAGTGGGAGATTGTCATGCCTTCTCTCCTTGTGAGATTGTTGATTAGAT  
1197 AGCCTGCCCTCAGAGGCCCTGCACTCTGTGTGGCTCCAGCAAAGCGTCAAGGTTAGCCAAGAATGGCCTGAAGTTACCTCTGTAGTGT  
1289 AATGTGGGTGCTGTTGGAAAGAAATGTGGAGGACTCAGCACAGCTCTGCTGTGCCGCTTTCAGGCTATGCCGTGGTTAAGAG  
1381 ACTAACAGAACAGCTGTGAGGCTGTTGAGGAATGAGAACATTCTCCTCCAGGAAACCCGGTGGTTAAATGCCCTGCAGCGAGCCACC  
1473 TTGGTCCATTGGAGGTCTGGTTACTTCTGCTCTGGACCTGATCTGGCATTCTCTCTCCTTGTGCTCTTAGGATGGCATTGG  
1565 ACACCTCTCACCTGATGCTGTTACCTTAAGCCCTGCTTTGTGAATCGAGCTGCCCTTTTTAAGCTTCACTGATTCTTGTGT  
1657 TTGATTCCAAAAGTGTACATCCATGTACAAAAGATAAAATGAGAGGGAAATTGAAATAATTGACATGAAAAGCCTCCCCACGCCCTCTA  
1749 ATCCCATCCCACAGAACATGACTTAACGTATAACAGCTCTGCACTTGTCTTGTAGAAACTTCCATGTTAATAGAAATTGTTAAATTACG  
1841 ATCCTGAAGGTTTTCCCACAAATTAAAGCGACTCCAGCTACAACAGAGGTGAGAATTTCACAAATGTTACTCTTCTAACTTGT  
1933 AGAGATACTGGGCCCAAAATGATTATTCTTAGCTCTGCTCTGCTGATAAAAGGAATGCCCATGGGAAATTGACCATTGTGTGGTGT  
2025 TGCTACCAAAGTAACAGGTAATGGGTGAGGTGATGCCAAACAATACCAGCTTGTGCTACTTCATGACTAAACTGCATGGGACG  
2117 GACTAATAAAATGAGAACCTCTGAATGATGCCCTTGCCTGTGATTTGGCAACAAATGAAAAGCAAATCAAATGATTATAATTGACTGCA  
2209 TGTTGACAAGATTCTCTGAGTGTGCTGAGGAAGCTAAAGGTATCTAAATTCTCAACATGAAGTATGTGTCTTCTGGTATTA  
2301 ATTAAAGTAACAACCTTTGAGTTGCAACCTAGAACATTCTATTGTATGACTGAGATAAAATTGCTTAAGAAACAACCAAAGAA  
2393 ACGAGATAACAGTTAGTGTGATCTTATCCAGGGAACAGGTATCTGGATGTTAACGAGTTGCAAGAACAGTTAAACTTGA  
2485 GAAAACCTCTGTGCTCCCTTGTCTTTAACTACTCTGGTATAGCAGGCACAAATATTCTAGGAAAGGCAAAGAAACTCACTAGCATTGTT  
2577 GGCTAAGGTGATGGGCCCAAGTGAAGTTGGTACAATTATTGTTCTTATAGACTCCACTTCTATCAGGTAAAGCCATGTACTCTGT  
2669 GGAATTGTGATGGGCCCAAGTGAAGTTGGTACAATTATTGTTCTTATAGACTCCACTTCTATCAGGTAAAGCCATGTACTCTGT  
2761 GCTTCTGTTAAATTGTCAGTGTATTAACTGTCTAATTAGCTGGATGAGTGAAGGTCTAACAGTGCACAGATTCTTCTATC  
2853 TGTGTTCTTAGGCAGAATAAGAGCAGAATTATTGTATTAGAGGCAGAGGGAAACAATTAGATTGGGAAAGTGTGTTATTTCATATG  
2945 GAAAAGTAATACCAAGTGGTAGGAAATGGCAGCAGCAAACGCATGCTGAGGGTGATTTACTGCACTAAATAATTAGCAGTATAAGT  
3037 TAACTATTAAAATAAGAACCTGGTGTCCATTCTGCCAAATATATTGAAATGACAATTACTAAATATAAGCATGGATAGTGGTGTG  
3129 CTTGTGTACATTTCAGTGGCACATGTTGATCTGAGCCTTACTGGTCACTCCATACATGTTCTCTAAATTGAGTTG  
3221 TGTCAAGAAAAGATTGCGGGTTGCATGTAGTTGCTGAGGATGACAGAACAGTAGTTACTAACACAGCAGAACAGAACAGAACATGAAGT  
3313 AAACGTGGATTTTAAAAATCAAAAGAACAGGCCAGGGCGACTGGCTCATGCCGTAAATCCCAGCAGTTGGGAGGCCAGGTGGCAGATC  
3405 ACAAGGTCAAGGAGTTGAGACCAGCCTGCCAATATGGTAAACCCATCTACAGAAAATACAAATAGCCAGGCATGGTGGTGCATG  
3497 CCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGGAAATCTCTGAAACCCAGGGAGACAGAGGTGAGCTGAGATCGTGCCTGCA  
3589 TTCCAGCCTGGCGACAGAGTGAGACTCCATCTCAAAACAAACAAAATCAAATAATTAGTTCCAGGCCATCAGGTATTGATGAAGTAGG  
3681 CTGGGCACGGTGGCTCACACCTGTAATCCCAGCACATTGGAGTCCGAGGCAGGTGGATCACCTGAGGTGAGGTTGAGACCAGCCTGGC  
3773 CAACATGGCAAACCCCGTCTACTAAAATACAAAATTAGCCAGGGCATGGTGGTGGCACCTATAATCCCAGCTACTGGGAGGGCTGAG  
3865 GCAAGAGAACGCTTGAACCTGGGAGGTGGAGGTGCAAGTGAAGCAAGATCGGCCATTGCACTCCAGCCTGGGGACAAGAGGAAACTCC  
3957 ATCTCAAAAAAAAGGAATATTAGAACATGTGATCTGCCATGGCAGGGACAGGAATGCCATGGGCTGAGCCGTCA  
4049 CTAGCTGATGCCCTTCTTGTGAGAACATCAGATCTGCGCTGGGATCTGCTGCTTGGCTCATGGTCTCCTGGCAG  
4141 AGCATCTCTCTTAGATCTTCTACCCCTTAGAGAGACCACCTGAAATCCATATTGCTGAAGCTATTAAAGTCCACAGAAACTTTCCC  
4233 CCCACTGTCTCAATTCTTCTACTGCCTGTGACCGTGCACATAAACACTTGAGTATGTGGCTTGGCTGACGACTACTTCTTA  
4325 GGCTTCTGACGCAGGCATCCGCCCGTGTGGCCTGAGAAGGGCTGGCTTGGCTCTGCCACCCACCTGCCACCTACA  
4417 CATGCACAAAATCCCTTCTGCTAGGTGCTAGGGTTGAATACCCATTGCTTACCTACTAATAGTAAAATTTCACAGCATTAGGTTATT  
4509 TTCTTGATTGATTCAAGTAAATATTAAACTGTTGGAACATGTGATAGTCCCAGCGACTAGATTGTTAAAATATTGCAAGGATCAATGAT

FIG. 12B  
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4601 TTGGTTGGCAGAAGTAGGTAATTCTAAAATTAAAAATGCAGGTAAAACAGGGACTGGAGAGGAGTATTTTCTAGTGATTAATAAC  
4693 CTTTATTTCTTATTGTTGTCTTACCCAGTTATTGGCTAAATCTGAGAACTTACTTTCCATGAGCAAAGTTAGAGGTAAC  
4785 TTAAACAAGCAGTTAGACAGAGGTAATGACCTTAGATTAAAAGGTTAGGTCAAGCTGTATAAGTGACTTGTGCTTAAGACATGATGA  
4877 GCCTCTGTTAACTGAAAGTCAAGCCCAGGACGCCAGCTGCCTTCCATCAAAGACATGGGATTGGTGGCAGCTGACTATTGATTCCAATG  
4969 ACGATTCCTCAAGTGGAGGTCTTACAGATGGCCTGTTGGGGACATTGTTAACCTGCGATTAACCGACGGCATCTCATCT  
5061 GGCTTTAAGCTCCTGTATCCTGACTTGTACAGCTTACTTATGCTTGTGCGACTATGTAAGTGACAGTATATGAGAAAGGTAGTGAG  
5153 TAGTAAGAATGTTGGAGACAATTAAAGCTACCATTCATATTCTATAAAAATTAGACTTTGTGCTGGTAAACAAACAGAGGACAGAGC  
5245 TTGTATGAAAGGATAAAAGAGCGTTAAGGGTACACGTCCATTAGGATAAAAAACTAGAATATTCTTCTGAAACCTGAAGCCCAGGCCG  
5337 GGCATGGTGGCTCACGCCGTAACTCAGCACTTGGAGGTGAGATGGGAGATTGTTGAGCCAGGAGTTGAGACCAGCCTGGCAAC  
5429 ATGGTGAACCCCCATCTCTATTAAAGAATAAGGCTGGGTGGCTCACACCTGTAATCCTAGTGCTTGGAGTGTGAGGCAGGTGGA  
5521 TTGCTTGAGTTCAAGGAGTTGAGACCAGCCTGGCAACATGGTGAACACCCCCATCTGTACTAAAAATACAAAATTAGGCGGGTGTGGTGGCG  
5613 CCCGCCTGTAGTCCCAGCTACTCAGGAGGCTGAAGCATGACAATCACTGAACTTGGGAGGCAGAGGTGAGTGACCCGAGATCATGCCAC  
5705 TGCACTCCAGCCTGGGTGACAGAGAGACTCCGTCTCAAAAAATTAGGCTGGCGCAGTGGCTCACGCCGTAACTCCAGCA  
5797 CTTTGGGAGGCCGAGGTGGCAGATCACGAGGTCAAGGAGATTGAGACCACCTGGCTAACACGGTGAACACCCGTCTACTAAAAATACAA  
5889 AAAATTAGTTGGCATGGTGGCAGGCCCTGAGTCCAGCTGCTCGGGAGGCTGAGGCAGAAGAATGGCGTAACCCGGAGGCCAGCTG  
5981 GCAGTGAGCTGAGATTGCGCCACTGCACTCCAGACTGGCGACAGAGCGAGACCTGTCAAAAAATAAAATAAAATAAAATAAAATAAA  
6073 ATTAAAAAGAAAAAGAAAAGGAAACCTTAAGCCTAGTTATTGAGGTAGACAGGATGCTACCCCTGCCGTCAATTAAAGAAGCAT  
6165 TTAAGCCTAATGAACACGAGCAGTTCTAATGTCGTTGGAGGGGAGGTAGCATTACAGTTCAAGATTCAATTAGCAATTACTGATTGAGC  
6257 ATCTCTGTGTCTAGTTATCTATGCTCTAGGCCTGGGATGTGGCAGTGAACAAGAACAGATGTAATGACAAGAGATGGATGGTGGT  
6349 GATGGTTGCACAATTGTGTGAATGTAAGTACTTAAGCCTAGTTATTGAGGTAGACAGGATGCTACCCCTGCCGTCAATTAAAGGTT  
6441 AATCCCAGCCTTGGGAGGCCGAGGCCGGGTGGATCACCTGAGATTAGGAGTTGAGACCAGCCTGATCAACATGGAGAAACCCGTCTCTA  
6533 CTAAAAATACAAAATTAAACCGAGCGTGGTGGCGATGCCGTAACTCCAGCTACTCGGGAGGCTGAGACAGGAGAATGCCGTGAACCCGGGT  
6625 GGCAGGGTTGCAGTGAGCCGAGATCCGCCATTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCTCAAAAAAAAGTTCAAATGG  
6717 TAAATTATGCATATTACAGAAATAAAAAAGGCAGTTAAGACAAGTAAGATGCTGTGTCATGGGCTAGATCAAGCACTTGGGTTGG  
6809 GTGTTAGGGACTTTGAACGGGCCTCTACCCCTGCGGGAGGCTGAGCTGGAGGGATCTGTGGGCCCTGATCAAGAAAGCAGGAGCTG  
6901 TAACCCAGCCTGGCTTGAACCTGAGGCTGCCAGTGGAAATCTGTTGTGTCAGGAAGGAGGCAGCTGACTGGATGGAGAACTGGA  
6993 GGGACTCTGTGGCTGCCAGGCCAGCTGCAGGGCACACAGCTGCACTCTGAGGCTGGCACCTGCCCTTCACTTACCAAGGCTTCTC  
7085 CTGTTTGTTCAGACGCCATCTGAGACGACAGGTCGATACATATGCTAACAGTGCTGCGAAGGCCAGAGGAAGCAGAGCT  
7177 TGTTGTTACAGAGGTAAGGCTTTCTGCATTAATTACATTGAAAGTCATTTCCTCTAACTGCCTCCTTTCTTAAATTCAAAT  
7269 TGTCAAGGAAGTGTCAAAGGGTAATTGTAATTCTATGATGGAAGTTCAAATAGAATAATGTAATTTCAGACTCTGAAACTTGGACAGA  
7361 AATGTCCACAGGGCTATTCTTTACATTTTATTATTAAACTTATTGAGGGCTATATCTGACTACAAAAGTGAA  
7453 TTCCACAGAAATTATCATGGACTTAAATAAGCAGTAATTGAAATTCACTGAAATCTGTTGGAGGTCTGTTATTGATACTGT  
7545 TTTAAGGGTACACACACATTATGATCATTTTACATTATATGCAAGTTATTGACTAGTATTGATACTGAAGTACTA  
7637 GCTGATAATAAGCAGGGCTATCGCTAGTCATATATATTATGATACTATATATTGATACTGAAATCATCAAGATACTGATTAAT  
7729 ATTATTGTTGAAATGCAAATAAAATTATCTTATGGAAGAAAGATAAAATTATTACTTTTATTATTATTGAGACAG  
7821 AGTCTGCTCTGTTGCTAAGCTAGAGTGTGGAGCAATCTGGCTCACTGCAACCTCTGCCCTGGTTCAAGTGGTCTCTGCC  
7913 TCAGCCTCCAAGTAGCTGGATTACAGGCGTGCACCACCGCCTGGCTAACCTTGATTTTAGTAGGGACAGGGTTCAGCCTGTTAG  
8005 TCAGGCTGGCTCAGACTCCTGACCTCAAGTGTGATCTGCCGCCCTGGCTCCAAAGTGCTAGGATTACTGGCATGCCACTGTGCCTGGC  
8097 CAGAAAGAGAAATTATTACAATTAGGTTGTTGCTTAGTTTCCCTGGAGTGTGTTTCTCCAGGTAAATTAGGTAGGAAG  
8189 GAATAATTAGATGTTAATTGTTCTTAAAGTCACCTCAATTAAAATAATGATTTTTAATCCTGGTTTCTAGTTGATATT  
8281 TAGATCATAATATGCTCATCAATAAAATTGCTTACTATAAGGAAGCTATAAATACTCTTATAAGACCAATTAAACAATATTAAATT  
8373 CCATTGAGATTGTTGAAAAATTAAATAAAATTAAAAATTTTAAAGTGTGTCCTCATCTTCTGAAAGAAGTAACCTCTGCTTACCT  
8465 CCTTGCCACTATATTAGTAAACTTAATTCCAGACAAATACAGCCAGATATGTTGTGAATGTAGTTATAATGCTTTAAGGCAGGTAG  
8557 TGGCAAACATATGACCTGCAAGCAAATCCAGCCTGTAGCCAATTGGTAAATAAGTTATTGTAAGCAGCCAAGCACATTGTTACA  
8649 TATTGCCATGGCTACTGTCACCATGCAACTCAAAGTTAAGTAGAGATAATATGACCCCTCAAAGCTGAAAATATTATGATCTGCCCTTAA  
8741 CACAAAAAGTTGTTGACCTATGTTAAAGCATGTGGAAAATTATTAATTGCTAACTCAGTTCTCCAGGTGATTAAAAAATATGGTT  
8833 TTTGAGGGAGAACTCTCCATTAAGTTATTAACTGCAAGGTTGAGCAATAGCTGCTTCATCCTATGCTGGAGCCAACATAACTAAC  
8925 ACTTTGGGACCCCTCCACTTGGTGGAGTGAACATCACTTCTCTCATCCTGATCCAGGGATGACCTAATGGCTAAAACAAAGCAA  
9017 AACAAAGCAGAAAAAACTCAAAACCTTCAGTGTAACTCAAAATATTGAAATTCAACCAGTTGAAATGTTAATCGTATAACTCAGT  
9109 CAGTCACATTCTGTCTTTGAAGGTACAGTCTCAGGATCTGGTTCTGATGGAACCTCTTATCTCTAGACTTCTGCACTCCCCAGAG

FIG. 12B  
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9201 GGGTGGGGTTGCTTGCCTAATTCTGTGCTTCTGCTTGGAAATTAGCCAATGCCTGCTATGTAGATGGTCAACACTGGCTTGTAAATCAA  
9293 TGAATCTCTAAATACTTAGCCAGGTTCACTGTGGAGTTTTTTTTTTTTTTGTATGTGCGATTCCTTATAATTATAAAATATA  
9385 TGAACATAATAAACTGTAATTATTTCCCCATTTGCCTAAGGTATTAATCCTGGCCAGGCGCAGTGGCTCACGCCTGTAATCCCAGTAC  
9477 TTTGGGAGGCCGAGGCCGGTGGATCACGAGGTCAAGGAGTCAGGAGACCAACATTGTGAAACCCGTCTACTAAAAATACAAA  
9569 AAGTAGCCAGCGTGTGGTGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGTAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGC  
9661 AGTGAGCCAAGATTGCACCACTGCACTCCAGCCTGGTAACAGAGCAAGATTCCGTCTAAAAAAATAAATAAATAAATAAATCTGGG  
9753 CTCCATTCTATAAAATGCATTTATAATACAAATTATGCTGGTTATTAGTTTAATTGGCAGGTACATTATACCTCAGAATAGTT  
9845 TAATGTCCCTGCAGGAGACTTGGTGGTACAATTCTAGTCTAGAGCTTGTGAAAAACCGCTGTAGCTCTTGAAGAGAATAGGATCACACCC  
9937 ACAAGACCACGTCGTACATAGTCAGGCCTGACTACTTAGCTGTGCCAGTGGACCTAGGGCAGTAGTGGAAAATCCAAAATATGGATTAT  
10029 TCTGAAATCTGACTGGTTTGGAAATTGAGTGTGAATGTATGATACTCAAAATGTGAAAATGCTTGTGAGAAATCTAAAAAAATCAT  
10121 TTTCAAGGATAAAATAGCATTAAATATTCTTAACACAGAGTAAAAAAATCAAAAGTTGCCAGCTCCAAAATCTGACTTTGCGCTTA  
10213 GCCCTTCTGCTGCATTATTCCACCTCTCAGAATAATTAAACTACATTACCTTCACATCACACATCACACCCCTGCCAGTAAAGTGC  
10305 TTATTGTAGAGCCTGGCACAAAATAAGCACTTGCTGCTGTGTAATTCTTACTTCATGAGTTGGAGGTGGAGGGAGTTGCTTCAGAAG  
10397 ACCTTCAGGCATGGCCTGTGACACAGATAGAAAGGTTGACAGTAGAAACGATGAAGTGAAGAAGCAGAATAGAGACGTTGTTCATGTTAGT  
10489 TACAGCCAGGCCAATAAACTAGATAAGGCATAAATACATTATCGACCTATGTTTCAATTGATTCACTCATGCTTTTCCACCCACAC  
10581 TGAAGTCTGACATAAAATAGTCAAGTGCTGACTGGACAGAAGATCATTGAACTAAGCTGATTAACTAAAATTCTTAGCTTTGATTT  
10673 GACTCATTCAATTGAAGATCTGGTGGATGTGGCATTATAATCTTAGGCTTATGCACTATTGGAGGTCTCATGGGTGGATGAACGACG  
10765 GACACCAGGCTGGCCATTGAATCTGTCATGTGGCAGGTAGTTGAATGCAGTCTGTGTAGGTGAGGTCACTAATAGAATCCTGGCAGTG  
10857 GAAGACTACATTAAACATTCTGTACACACACAGATGAAAATGTATGGCTAATATTAAACTAACAGAGCTAGCTAGTTCAATATTAGTAA  
10949 TCACTTTCTTATGAATGGAAAGAAAAACTGAGGGCAGATTATGGTAATATTAACTAACAGAGCTAGCTAGTTCAATATTAGTAA  
11041 ATACCATGAAGGCGTCTTAAGTTCACGCATCCTATTCACTTTATGTCATAGTAGAGGCCACATGGTTTTAAGAACCAAGGTGCTTACTC  
11133 TGAAATAGTCATTGTTAAGTAAATGTACAAGGTTAGGTGAAGTTGTCTCCTGTAAAACCTGCTCTCAGATCATTATGATGATAACTTA  
11225 AAGTGTACTACCCCCAAGGGTAATGTTCACTGGTCAAAGTCTCAAGCTCACAGGAATCTCTGGTGGGAATTTCAGGCATTAGCTG  
11317 TTGATGGGAAAAAAATTTTTGATGTTCTATGGGTATGCCCTCACAAACTTCCCAAGTGTGTTCCAAAATCACGTCTTCTGTTTTA  
11409 TTTCTATTAAATCCCCCTCAATAGTCATCAAAACCTATAACTCTGACTGGCATTGTGAACTATAATATGAAGATTACTCAGG  
11501 AGAGTTGACAGCTCCGAAGTGAGTAAGCTATATTACACATAGGGAAAAGTCTTGACTTGAAATGCTTGGGGAGGTATGTAAC  
11593 TCATATGCAATCAGAGTAATTGAGGAAATATTAGTGGTTATGTTATGTTGACTATTGTTACAGGGCCTTGATTGTAAGA  
11685 CTCAAACATGCTACTTGGTATTGATAGGTAGTAATAAACATGTGGATGGTTAATTATGCCAGTGGTCTTTCAGGGTACCACTGATAA  
11777 ATAAATAGGTGAAATTTCACACAAACAAACAGTAAGTGTACTGAAATATGCTGCAGTCATTTCCTGAAAG  
11869 AATATTGAGAAGATAATTAAAGAGCAATTACATTGAATAATTGTTAAAAAAAGTAAATCAAGAACAAAGCATTTC  
11961 AGTTAAATTGTTTATCTCCTTAATGTATTAACCTATTCTAGACTATACAAAAGCAAGTGTATTAGATTGAATAGTTGTGGCCAAA  
12053 GTGAATCGCGTAGCTAGGTATTGCCCTGACAGACTATCTTATAAAAGGTTCCATTGTGTGTTGCTTAAAGGAATACCTGAGACTGGGT  
12145 AATTCTAAAGAAAAGAGATTATTATTATTAGTTGAGACAGAGCTTGCTCTGTCACCCAGGCTGGAAATACAATGA  
12237 CACGATCTCTGCTCACTGCAACCTCCACCTCCAAAGTCAAGCAACTCTCCGCCTCAGCCTCCGAGTTGCTGGGATTACGCCACTTGCC  
12329 ACCACGCCCGCTAATTGTATTAGTAGAGACAGGGTTCACCGTGTGCCAGGCTGGCTCGAACCTCTGAACCTCAGGTGATCCAC  
12421 CTGCCCTGCCTCCAAAGTGTGGATTACAAGCATTAGCCACCGAGACTAGCCAAGAAAAGAGATTATTCTGCTTATAGTTCTGAGGT  
12513 TGTACAAGAACATAGCACTGGCTCTGCTCAGCTCTGTTGAAGACTTTGTGCTGCTTAAACATGATGAAAAGGTCAAAGGGAAAGT  
12605 TGGCACTGTGAAAAGAGACCAAGAGGAGGAGGAAACTCACTTATAACAACCCATTCTTGGGACTAATCCATTCAAGAACAGTAA  
12697 TCCCATTGCCCAGGAACAAGAACATTCACTCATTACTGTGAGAACAGCCACCAAGCCTCTCATGATGGATCTGCCCTAAACCCACTAGGCC  
12789 ATTATGCAACAAACGGGACCAATTCAATCTGAGTTGGTGGAAATAAAACATATCACAACCATAGCAGTGGCAAATTGAATTATAC  
12881 TTGATTTGGAAAATTGAAAGCAAATAGTGATGGATTATGTTAAAACATACCATCAGCAATTGAAATATTACTTGAGACCTGATTAATG  
12973 TATTTCTTGCCTTGTACATCTTGAGCTGGAACCTTTATGCCGTTCTCAGTAGACCTAGCTGTTGTTTCTCCTTGTGGCT  
13065 TTGCCACTCCTTAAGAAATGTCGCCAATTCCCGATTGCCCTTTAAACCTCAGCCAGGAACACTCCCTCTAGTATTCTCAG  
13157 ATGGGTAGCCCTTACTATATTACCAATCCTCCCTAGGGATTTTAACTCTCCATTGGATTGGCTTAACCCATCTTGTGAT  
13249 CCTCTGTTCATAGTCTCAGGGTGAAAGATATCAGACTATGTCATGTCGTATACTTACTATCTAACAGTGTGGTACATTCTCTCT  
13341 GGCATTAATGAGAACATTCCAAATGTGTGATGAGAACAGAGGAGAATTGTAACAGTGTGGTAAAGAACACAGATTCTGTTCTGCC  
13433 GACTCTGCCGTGTCAGCCTGATTCTCATCTGTTAAATGCCCTAACAAACAGTCACCATGATTAAGGATTAATGAGAGGGCACATG  
13525 AGAAGTGCAGGGCTAGCACGTCAACCCATTGAGTAAATGTAAGCTGCTTATTGGTATTGGTCTTGTGTTGTTGTTAATACCA  
13617 TCATTGTTAACGGTTCAACGCAACAACTCAATCTCCTTTTCTCATAAACTTTGTATTAAAAGTTATTCTACCAAGTCTTGTGTTA  
13709 TTAAAAACTAATCCACTTCTTATTAGTATGCCCTGCTAACACTCCCCAGAAGCTATGCTGCTTTCCACATAGCTTGGAGCTTCTT

13801 ACTCAAGTCTCTGGCTTACCCACCTTGAAGGAAAGCAAGGGCATAGATGGTTTATTCTTGTCTGAATAAAGAAGCTGGCCATCTTGGATT  
 13893 TAGTAAAGGCGGGCCCTATGATGGAGGAAGAAATGCAAAGCCTCTCCTGACTAGGCATTCTAAAACAATTCTTGTGTTTTAT  
 13985 AGCAAAGTGGTCAAGTGGATAAAACTCCAGTCATGTCTATGAAGTGTGACGAGGAGGTGACAAAGATGAGGTGGGATACCTGCTTGTGT  
 14077 TGCTTCTCTTCACTCTAGATTAAACATCAATTACAGACTTAGAAGATTAGTTAGAAAATTACCGACATTAGCCAAAACAGGCATTG  
 14169 GAGTGTACATGAAACGGGAATAATTAAATGTTATTGATTGAGTGGAAATAAGGCTCTGTTCAACTTACTGCTTAGCATTTCAT  
 14261 GTTCTCTGGTTGTGTTATTGTTCTGAGATCATTCAAAGACTTGGATCAGATCTGGCTACATTGTTAAAAGATATCAAGATGACTTAG  
 14353 ACCTTGAATTAGGTGTTTCAACAGATCTCGAAACAGCTGCCAGCCAGTAGATTAAATGGCTATTCTCAATGATTGCTTTAGTGA  
 14445 AGTCTGATTGATCAAGCCCACCTCCCCATTCCAGAGGAAAGCTCATGGCTAAAGAACTATATAAAGGGAGTAGGGCATTGAGATGAGTC  
 14537 TGCCCACTGAGTGAGGGAAACCTCACAAGAAGACAATGCCATCTGCATTCTCATCCTCCCCATTGATTGTTAAGTGTCCCATTGTGAG  
 14629 TTTAGGTTTCTTCTTAAAAAATTGTCAGCTGAGCTATAACATTAGCCACTCATTAAGCAATGTGATGTAGCAAATTATTTTATT  
 14721 CCCCCATCACTTTATCTCCTTCTGTATTGCCTCAATTCCCTCCCTGCTTATTCACCTTCCCTGAACACTAACGCTCTGGGAAGGTTTC  
 14813 CAGGAATGTGCATGTGCTTTGTCTCTGACTATAGGGGAGTGTCAATTGAAAACATTTCGTGAAACCAGGCAAGACCTCAACGTGA  
 14905 GTGGTCAGTTGAGGTATGCTCTTTGGCTCTTGTGGCTCATTAAACACTGACAAATAAAATTGGACAGGAGCTAGCTTGCCTTAA  
 14997 TGGAAATAAAGTTTCAAGAAATGTAGGCAGGCTCTCTTACCGCTAAGTGGACTTTATGTGACTTGTAGGCATTGGTGTCAATGGGTG  
 15089 CTTCAGTAAAGGGCAATGGACAACCTGGCACAAAGGGATGACCTCCATTGACCAAACACTCACAGCAAGCAACCCAGGTAATAACGGGAG  
 15181 GTTGACTGCTGGTGTTCCTCTCCTAGGATGCTGCCTCCCTGGTCCCAGAAGGGGGATCACCAAGCATTGGCTGGCTGTACAAAG  
 15273 GCAACATGAACAGTGCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTGCCTCCCTCACAAGCCTTCTGCCATAGAGCT  
 15365 CGAGAACAAATGCTCAAGATGAATGCGCATGCTCTTCCCCACAAAAGGGACATTGCTGATTCTCTAGGATGCTCCCTGGTGTAGCACC  
 15457 CCCATTGGCACAGCCTCATCCACCCACTTCCCTACTGTCTCTGACCAACCAGCATAAGGAGACCATCCCTGGCTGGTGTAGGTGAG  
 15549 ACACGTACATAGGCTTCTCTGTAAACTGAAAAGTGTCTTGGTACCTCACAGAATGTACCAAGGGCTATCTGTATGCCAATC  
 15641 CTGAGCACTCTGTGGAGGTGTACTGCAGCAAAGTCAAGTAAAGCAAAATTGAGGACGAGAAAAGAAAATAGTGCATAGAAGAGAAGGTT  
 15733 GCAGACAGAGAAAGTCAAACCAATAGAAGAAGCTATTAGGAGAAAAGTGGGACCAAGGAAACATCAGGATTAATAACAAAGGGAGAGAAC  
 15825 AAGGGAGTCAGGGAGATAAAATTAGGAGGAAATGTGACTGTCAATTACCTTAAGGCTGGAAAATCATTAGCGTCATGAGGCAAAAATAG  
 15917 TTCCCATTCTGTGAGCAAGAAACCTGGGATTTAGAGAAAGTTCTGTCTCTGTGCATCCAAATTGGAAGTCCCTGCACTGCTT  
 16009 TTGGGTAGTTATGAAAATCTGTATTCCGTGGGTGAGAAAATGACCATGGATATTAGGGGACCACTCCTCAGAACTGAGATGCACTG  
 16101 AGCTTCTTAGATGGATGGGAGTCTTGACCCCACAGTGACCTGGAGCATCAGCTAGAGTGTGTTATTTCTCTCAGTCATTAAAGAGACGA  
 16193 GTCATAAGTGGTTATTGATAGAGATTGTGACCCCTCTCATTGAAAGAATAGCTGTGTATATTCTCTCAGTCATTAAAGAGACGA  
 16285 TTTTCCACCTGATTCAACTGGCATGGATCCTATAATTGAATTTTATAAGATGAAAAGATCTCAAAGAACCAAAAGGATCAATT  
 16377 TCTGGATTCCGTATGGGTGTCGTTCAAGTAAATATGAAAAGAGTTTACCATATGTTCTTATCTGCAGTAGTGCTTATGTGTAAATT  
 16469 GCAGATTAAAGCAAACACTCCAAAATGCAATATGCATGGTAGAAATATAACATATAACTTAAATGAGGCAAGCCTGTTTCATCAT  
 16561 TGTAGAAGATGGAAGGGATAATGTAGAGCAGAATTATGCTGTGGCAGGCAGGACTCTGGCTGCCACTTATAGCTGCGTGCACCTT  
 16653 AACAGGCTACTTAATTCAAGATAATGAGAATGTTCTTAATACGGAAATGAGTACATTGGATGAATCAGTGCAGGAAAATATTAAAACAC  
 16745 TTCATAGTATCTCAGTGGTATTTCATCGCTAGCATTGTAGTACAGTGGCGGTGTAGATCAGTAAAGAGATTAGGTTCAAGCGCAGATTG  
 16837 AGTTCAAATCCCTGCTCCACTTACCAACTGTGTAACCTGGAGATGTTATTAAACCTCTGTACCTCAGTTCTCATTTGTTAAATA  
 16929 AGGATAATGGCAGTACCAAATATGGTTACTGAGAGGGTCATTCAATTACACATGTAAAAGCTTAGAACAGTGCCAACAAATGTAAGCATT  
 17021 TGGTCAGTATTAGATAGTTGTTATCATAGGGCTGTTACTTTATATCATAGGGCTATGTACTTATCCTTAAAATTATTGTTAAATT  
 17113 AAGATAACACATGAATGTATTTCCTGTAAAAATCAGCCAATACAGATAAAGTGAAGTCTCTGGACTCCTCCCTTCAGTGTCT  
 17205 CTTTCTGAGGGAGCTACTACCAGTTGCATGCATCCTCTGTAGCTTTAGCATTGTCTTGGAAAGAGAGTTGTCAATTCCCTGTCC  
 17297 ATCATCTGTCCATCCATCCATCCATCTGTCCACCCCTCCATTCACTCAGCCTGCCACTTCAAGGAAGATTAAAGCAGCAG  
 17389 TTATAAGCATAACAGGACATGGGATAGCATAAATTAAAGTGGGGTGAAGCAGAAAGATGAACAGGGGATTGGATAAGGGTGGAGAGAA  
 17481 AATAGAGTTAAGGAGAAAGCGTATGTTGAAGATCTAACACCTGCTGTGGGTGGCCACCACTGGCTCTATGCTTCTCACTGGAGAC  
 17573 CTGTTAGTCACCGAATTCACTGACATGAGATAAAGGCATGATGCCTGTTAGTCAGCTAGAACGACCCCTGACTTTAAAAGAAGT  
 17665 TAAAGCAAACAAATGTATTGGCAACCTCATTAAAGTAGGAAGTAATTATTGTTATAAGAGAGTTGTGCTGCTGTTCTG  
 17757 GCCCAGGGACAGATGTTATAAGTACAACCTGCCCTGAGCTATCAATTAGTCTCCGGGTGCATTCAAAATCTAAGGTTCTGACTCAATGG  
 17849 AAGTCTCTCCTCAAATTGCTTGCAGATGCAGCTGATGGTGTTCATTAAAGTGTATCCAAGGCTCAAAAAGTAAAATT  
 17941 TGTTTTATCTGTGCTGTTGTAACACTAACGATCAAAGTTGATTTAAAGTGTATTAAAGTGTATTAAAGTGTATTAAAGTGTATT  
 18033 TAGTTGACTGGTGTGTGAATTAAAAAGTGCCTAAACTAAAAATTGAGCATTGTTAGAACCCCTGAAATTATTACTTATTTG  
 18125 AGATGAGAAAATGAGGCTCAGAACAGAAATTAGAATTGAGGCCTAATGTTCTCCACTTTAACCTCTTCAATTGATTGTGA  
 18217 GTATGCAGGGAAAGGAGGAGAGAAAATTCAATTGTTCAAGCCTTGACTTCTCCCTGGTCTGCCTGAAAGTTAAGTGGAAATCCAAA  
 18309 GTGGCAATTACTGAGCCCACAGCAGACAGTCGTGACAAGAGTGTGGCTTGCCTGAAAGGGAGGACTTGACTTGCATTCTAAGAACTG

FIG. 12B  
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18401 TGCTGCAGAACATCACAGAGACTTTGGGAGGGTTGCCCTGTCCTGAGACCTCCACCAAGGAACCTTAGAGAGAGTGAGATAACCCAGTAG  
18493 GATTAGTGGCTATGCCGGGGCTGTCCTGCTGGCTCAGGTTAGTGGGAGTGTGATTCATATCGCTCAGGCTGTCCTACAGGGATC  
18585 TTGTGCCATGATCCTCAGAGCTGAACCTCTGTCTACTGCGGCCAACCTGGGAGATTTGCTCCCTGGAGGACATCTGGAATGTCCTGAAGA  
18677 CTGGCATCTATTGGCTTAAGGCCATAAATTGCTAAACATTGTACAATGCATGGACCAGCCACTCACAACAAAGAATTGGCTGCCAAGTG  
18769 TCAGTAGTACCGAGATTGAGAAATCCTGGCCTAGTGCATGTCATCTCCGTCGTTACTGCACATGGACTACTGTTCTGTTCTGAGCC  
18861 AGTCACCCCTCTGCAGGCATGAAAAGTGGAGGCATGAGGCAAGGCCACGGACAGGGAGTCCAAATACCTTTGGGATTCAAAAGGATGGGA  
18953 AAGTCCAGATAAGTAAGCCAAACATAGTAATAGATAATGGTTGGCTTTAAAATGTAATACCATACTACTTCATTAAAAAAATAGGAG  
19045 CTGAAGAAATATGAAAATTTCATGAAATTTCATTCAACAAATATTTCAAATACCCACTATGTGCAAGTCACTGTAGAGTCATA  
19137 GAGACTAAGGATGTGACTGACAAAAATGGGAGCACTGAGGAGGTTCACTGCAGGGACACACAGTGAATCAGATGAGTATGTA  
19229 AAGCAGGTAAATGAGTCAGAAGGAAAATAAGCTTGCAGAAAGTGAAGCAGGGAGGGTAATGGGATTTCATGGGGGGGGCTTTC  
19321 ATGAGGAGGGGGCAAGCTATTAAAATAGCTTGGTCTAAATGCCAATGAGATATCACTCACCACAAAGAGAGAGTAATTATTTAAAGCAG  
19413 TTCTAATTCTTTAAAGTATGTCGTTATCCTTTTCATTCAAGAACAAAGTCAGGCGTTTGCTTTGAGCTCAAGATGCAGGACA  
19505 AAAGTAGTTATCTCTGGCAGCAGACAGTGAAGTGGAAATGGAAGAATGGATCACAATTCTAAATAAGATCCTCCAGCTCAACTTGAAGCT  
19597 GCAATGCAAGAAAAGCGAAATGGCAGCTCACGAAGGTAGATAGGCTTGGCTCCCCAGGCACATAACACTCTGTTGGTCTTTATT  
19689 TTGCCAGGTGGGTATAAGAAGGAGACCTGTTACACAAGTACATGAGAGGTGGGACGGTAGGGAGCTTTACAAATATCCTGTCAGCAAA  
19781 GGTTTGTACATTATAACTTACCTCCCTGACATTCTGATATGAAATCATGTAATGGGAAGAACCAAAGCTTGGAGGCAGAAAGGGAGA  
19873 CCTGGGTTTGAGTGCCTAAATACTGTATTCAGCTGTAGCCCTGGTAAACAACCTATGTTCTGAGCCTCAGTTGACTCACCTATAA  
19965 AATGGGAATAAACATGAAAATTGCTGGGAAGATGGGAAGTGTAAATAAGAAAATGAATCTCAAGTATCTGCATAGAATTTCAGTATTAT  
20057 AAAATATTAGTAATAATTAGAATGCATGGGAGCCTCAGATTAAATTGGTGGAGAAAATCTGGCTATGTTCTGACAATTGTTACTTC  
20149 AACCTTAGGTGATTCCCAACCCCTGGCTTCCCTAGAAGTACCTGGGAGCTTTAAAATACCAATTACCTGGTCCACAAAAGATTCTG  
20241 ATTTAGTTGGCTGGGGTGGAGCCTGGCAGGTCTGACTTTAGGGGGCTCATGGACGTGTCATGTGGCTGTTGTCATAGCTAGTGTG  
20333 AGTTCTAATTGGACGGTGTCCATGCTATACCAAGCTGCTCAGTGTGTTGACTTCATCACTGAGCCTGTGGATCAGTATTTTCAAAGCACC  
20425 CCAAGTGTTCAGGAGCATCCAGAGTGGGAACCACTGTGTTCAATTGAAGGCACCTAACAGAGAACGGCCTCCTCCTGTTCAAAT  
20517 GAAATGCTATGAATTACAAGTGATTCCGATAATCTGTTGCAATTAGATGATGAACAAAGCAAATTGGAAGGTTCTGGTCCGGTTAG  
20609 ATAGCTACCTGCCGGAACTGCCAAGTAACATGCTTATATCTCTGCTCTGCTGAATGCTGTTGAAGTATGTCATTTCACTGGTT  
20701 TGTCCAGAATGGAATCTGTTGAAATCATAAAAATTACATTGTGATTACCTCTCTTTCTGACCTGATTACGAGGTGACGTGACTCATG  
20793 CAGTATGATTTCAGGTCTGCTTCTAAAAAGTACCCCTACAAAGCATTCTCTTTATTATTATTTAAGTGTGTTCTCCCTGATAATGCTT  
20885 AACACTGCATCACAGGTACTGAAGAAATAACTGAAATATGCAGGCAGATGTTCTCATATAGCATCGTACTTCTATGTTGATACATGTGCT  
20977 CTCCCTTAACAGGGTAATAGACACGGTCCAAAGAGGAAGGACCTGGTAATCTGCCCCAGAAACCCGGGGTTGCCTGAGTTACAGAAATT  
21069 GTTTCGGGTCACTCTACTGGAAAAAAATAAGCTATTCTGTGCTTACAATTGAGAAATTAAAAGTTACTGAAAAGCACAAAGAAAA  
21161 GCAAATCAACCATACTGCTACTCCAGATTAAATCTATTATGATGTTGCCTTTAGCTTCATATTCTAAAAGATATAAACATCGG  
21253 TTATAGTTGAAGTTCTTTAAACACTGTCCTTATTCCCATTCTCTCTCCACAACCCCAATCAGAACAGCACTATTAAAGTTT  
21345 ACTTTCATTTATATCTTACAAATAATCTACATAATGATATATACAGTATGTTAGTATGTTAAAAATGTTTATAAATGCTAAC  
21437 TACCATATGTATTCTGCACTTAAAAATTAAATTACCCCTTTATTGTACTATAGACTTTATTAGCTGTTCTATTATTT  
21529 CATTTCCTTCTATTATAAACAAAGCTACATGACTGTCCTTGACTTGTGTCCTGTGTATCTGAATGATTCTTCTTAAATGAGAGAAA  
21621 TATCTTGCTCTCTAGCCCTTGCACTCTACTCTGTTACTGCCCTCTATTCTTTGATACTAGAGTGAATGGCGACCCCTCCACAC  
21713 CCACATCTAAACACTATAATAGAAACATGGTTATCTATATAGGATTATAAAAGACCAGCATTGACCTTATTAAAGACAAC  
21805 ATGGCTGTTCTCAAGTGAAATCTCCCTCCCTGGCTAGGGCTTAGAGCATTGTTCTTAGGACTTGACTGCTACCACAGTATCTTT  
21897 TAGCACCTGCCTATTAAAGCTAATTAGTGTGCAACCTGTTAGTAAACCACCTCCTAGTCTGGGAAGAGTTGGCTGTTGTTGTTATGA  
21989 ATGTCGTGTATCATATTGCTGAGATTGCTTTGTTCTGGATGTTGGGGTCATAATTCTCAAACAAACAAATTGTC  
22081 ATTGGGTTTAGTTGTTGCAGCAGGTAATATATGATGCCATCTAGAAATTCAAGAAAGTAACCTCTGCACCTACTGGGTGAACGGAATG  
22173 GATACCTAGGAGAAGATTGATGTTGAGCTTGTGATTAATTAAATCTATGCTTTCTATGAGGATATACAGGAACGGTCCC  
22265 CTCCTCTTACTACCCAGCCAATATAATTCACTGATTGTTGATCCCAAGACCTAGGGAGATTTTAAGATATACATATATTAAATATAA  
22357 ATGTATACATTATGTATATACCTTTATAAGTATAATTGTATATTGTCATTAAATTTAAACTATTGGAATCTTAAACTATGGGTTA  
22449 CAAGTTAGGTTAAGCCATTAGTGTGAAATCAGTTGATTCAACCCCTGCTTGTGTTCTATTGTTCTATTGTTCTATTGTTCTATT  
22541 TTATTGAGGTATAATTGCAATAGCAGAATGCTCAAACATGAATTGTAGAGCTACTGGAGTTGCGATTGACTGATATAAGCAGCCCT  
22633 CAGGCTAGCTGTACCTGAGACCCCTTTATTGACCTCCATCACCCTAGATTGACTTTCTAGACCTCCTGTGAATGGACTTA  
22725 TACATGTTACTCTTGTGTCAGGCTTATTAGCTAAACATGTGATTCACTTAAGAAGTTTTAGGTGGCATAGTGGCTCATGCCTGT  
22817 AATCCCAGCAGCTTGGGAGGCTGAGGTGAGCGGATTTGAGGTTAGGAGTTCAAGACCAGCCTGCCAACATGGTATAAAACCCGTCTC  
22909 TACTAGAAATACAAAAATTAGCTAGGCAGGTGGCAGGTGCTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCATTGAACCTG

FIG. 12B  
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23001 GAAGGCAGAGATTGCAGTGAGCTGAGATCATGCCACTGCACCTAGCCTGGGTGACAGAGCAAGACTGTGTCTAAAAAAAAAGGGTC  
23093 CGTTTAATGAAATAAAATGGAATGGAGAATATGAAAGTACACTGCCCTAATAATGACATTATTTTATATAAAACTGTCAATTAT  
23185 TTTGGTGGCACCTGCCACCATGCCCTAGCTAATTTGTATTCTAGTAGAGACAGGGTTTATACCATGTTGGCGAGGCTGGCTTGAAC  
23277 CTAACCTCAAAAGATCCACCCACCTCAGCCTCCAAAGTGCTGAGATTACAGGCATGAGCCACTACGCCGACCTGAAAAAAACTTTAA  
23369 AGTGAATTACATAATTTCACATAAAATGTCAATTAAAGGGCAATGTACTATTATACATATAGTGTATGTTGTCTGCATAGT  
23461 GATATAAAAGATATTGTTCTTAGTGTCTATTATGTATATTACTTCATTGGTATATAATGTACCTATTGGGAGTTCATGT  
23553 GATACTTGATATCTGTATACAATGTGTGATGATCAAATCAGGATAATTGGGATAGCCATCACCTCAAACATTATCTTGTGTTGGAAATT  
23645 TGAAACATTCTTACCAAGGAGTCATGGTAAAACCTGAAAAATGAATCCTGTTAGAGGTTTACTCTTCCCCCTGGCTTCAAGGTGTT  
23737 TACAAATACTTTATTAGGAAGGTAGAAAGGTGAAAGTAATTGGAGGGAAAAGAATGAAGAAAATGGAGATGAGTTATTCACTCA  
23829 GCACATGGGTATCTGGGCTTGCCTTAAAGGCCAGCTGGTGTCAAGTGTGAGCAGGCCAGGCAGTAAGGGAGACCTGTGTTCCCCAT  
23921 CCCCAGCCTTGAGCAAAAATGCAGTTGGCTGTTATCATCCCCCTCAGGGTGTCTGAACATATTGACCCGGTTGAGAAGGCAAAGAAGT  
24013 TGACCTGATAACTGTTGGTCATCCCATAGGAAGGATGGATTCCATGGTACAGAATCAGAGACTGAAGTATGCAGAGGGAGGGTGGGAGG  
24105 AGAGAACTGTGCAAGGAGTTACCCAGGGTATGAAGAGGTAAAGAGGTCAAGTACAGGGAAAGGTGCAAGAAAGGGTCAGGCTGGGAGG  
24197 CTGGGCCACAGTCAGTAAGATTACAAAGAAGGGCTAGAACATGAGGGCAGGCAGAAGGTGGCTGAAGGTGTAATTGACGGTTCC  
24289 TTTCTAATCAGCTCCTCTAACCTCCTCATCCTGTTGCCCGCTTTGTTCCACTGTGACTAAGACATAGCCAAACAGGATATGACCG  
24381 ACAGGAAGTTGTTCACTGCAAAAATAACTGATGTCTCATTCTGAATATTATGGAAGGGCTATTACTACAGTGTGAGTGTAAACCC  
24473 AGGTTTCAGAATATTGTATAATCTTGGAGCTATGTTGACATTAGTACTGAACATCTGTATTGTTCTTATTAGAGAACACACTG  
24565 TATTACCCCTAAAACGGTCTTTCCCTATTGTCTATTGCTATTATGGAACCAAACAATTATTATTGTAACAGTGTGAGCATCAGTCT  
24657 TATAAAATTTAGTTGATACACAAACCGTAGTTCAAGTTAGTAAATTGATTCTTCCAGAAAGTCAAGGAGTAACATAATCAGGTTAT  
24749 AAACCTCATTACTAGTTATTAAATAATTCTCTGGTTACATTATCTTAGGTGACATCAGAACATATATGTCACCTCCTAAAGAT  
24841 AGTGTGAAGAAAACCCACCTTATGTTCTTCCACAGCTTCTGTTGAGCTTTATTGTACTCAAAGAATAGCATCCAACTTTA  
24933 CTTGGTTCCCATGTTCTGAAAGAGAAGTAGAATTCTTCTAAATCCGAATTGTCACATCCTTACCTTTAACTTGTAA  
25025 GCAAATGAACCTATTGTCAGGTAAATCTTCCACAGITGCATGCAGGGAAAGTATGATGTCTCAGACTTATAGTCTCATGGAGATGGGAG  
25117 TGAGGATCAAGGCCATGCTCAGCAGACTTGTCAAGGACCCAGCAGTTCACGGACACCTTTCTTAATTAAACCAAGTCTATAAAAG  
25209 TGCTTCTCCCTAGATTCCAATCCAGAAAACAATATCATTGCACTATTATACAAAGGAGCTGGCTAGGTTGTCTGTGGGTCAGCTGG  
25301 TGTTGCATTCTGGCCTCTTGTGAAGAGGATGAACTGATGGCCTGAGAAGTTAGGTGTTGGAAAGTAGTGGAAATAATCATGATAA  
25393 CTCTTAAATTAAAGATTATATTGGCCTCAAAACATTGCAAAGTCCCTATTCCAACCCAACTGTAAATGACCCAAACATTCA  
25485 ACACATTGTTCTGATAATTCTCAGAACATAAGATGCTGTTGCCATAATTGCTCTAGATTGTTATCTACTCGCAAATAAAATT  
25577 AAGACACAGAGTATGCCCTAACGCAACTTCTGAAAGAAACTCTGAATGTTGGTCATAACTACTCTTAAGACAAAGAAGAAAAC  
25669 CTTGTCAGGGTGTGTCATTAGTGTGAATGTAGGTTACAGGATGGGTTGGGGGGAAATGCCCTGGTTAGATGAATCATTCTT  
25761 TCCTTGTCTCTCAGCAAACACCAGTTCTACAGAGAACAGCTCTGCCATTGTGCATTCTGCTCCATTCTCTCATTCTCTCCA  
25853 CGAAACCCAGAGTAGTCAGTGGCTTGGCAGGAAAGTGGCAACAGGGTGTCTGGGAAAAGCCAGTTGGCTTCTTACCATCACAATAT  
25945 AGACTGACCACAGGTATTAAAGAGCAGAGCTGGTTCCACTCTGAGAAGTGTCAACTACAGACTTGGGATGATATTGTTATAGC  
26037 TGTATTCTCCACTCTAGATTGTGAAAGTACATATTACAAGTATTATTATTACTAAATTAAATTAAAAGAAGCGTGCT  
26129 TGCCGAATAAGTAAAATACCCAAAGTGTAAAGAAAAGTCACCTTCCCTCATCCTCATTCCCACATTCTGAGAACACTGAAG  
26221 TTAATAACCGGGTGCAATTCCCTTACCAAACGATTGCTCATAGAAATATAGATAAACATATGTAAGGTTTAAGTTTTAATAAA  
26313 AATATGTTCATGATATACATTCTGAAATTCTGTATCACTAAAAATATTCTAGATGTCCTCTGGCCAGTGGAAAGATCTGGT  
26405 TCCCCCTACATACATCAGCAAGCTGCATGATATTCAACTATTGCTACTGCACAGTTATTGCCATCTCCATTAAATGAACATT  
26497 AGGTTTTCTCAGTTTCTGCTCTACAAACAGTACACAATAAACATGACATTAAACTTGTGCTCTATTCACTAGTAGGAGAAATT  
26589 CCCCCATGTGGATTAAAGTCAAAGTTATTGTGTTTAATGCTTAAACATGCCAGGTTACCGTCCAAAAGGCTATAACAAATT  
26681 ATTCCTGTTCTGCTGCATCTCAGCAGGAGTGTAAATGGTATTACTGTGCTTCAATTATATTGCTGGTTATTAGTGAATT  
26773 CATATTTCATATATTATTGCCATTGTGTTCTGCTGCTGTTCAATTGTTACCTTGTGTTCTGCTGTGTTAGT  
26865 GTAATAGTTAGACTCTGAAGCCAGGCAACCTGAGTTAGAACGCCAGGCTCTATTGATGTAGGTCTTGGGAAAGTACCTAACATT  
26957 ATGCCTTAGTGTCTCTTAAATGAGCAGGGATAATAATAGTACCTGCCTCTAACGGTTATAAAATTAAAGGGCACTTAGGGTAAT  
27049 ATCTAGCAGGTAGATATTGGCTATTCAATAGTAGCTCTTACGTTACTATTCTCAGATACTGTTCTGACTCTGGGCAAAGTCCTG  
27141 CTACCCCTGAACCACATTTCACCTCTAGATTACTGGTAATTCCATGCCACTGTTGGGACTCTGTGTTAAATGCATCATCT  
27233 TAGACCTTAGGAGGGATGGGAGGAACCTTAAGAACGCCAATTGCTTTATTATCTGTAGCAGAGCAATAGTATATTAGGTAGATT  
27325 ACAAGCTTTAGGTTATTTCATCTAAAGCTGCCCTCTTCAATAATGATGTCTGTGGTAAAGAATATCTGTTGGGTGTTAGT  
27417 GACAAAATCAGAACATGCTTGTCTATTGGCTAGTAGTTAATTGTTTATTGTGCTGCATTCTATTGTTCTTAATT  
27509 CGAGCTCATTAGCAGTTATTCTGCTTATTCTCTAGCATAGTCAGCTCAAGACAAAGCATCTTCAGAAAGCCACTAG

FIG. 12B  
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27601 GAATTGCATCTACATTAAGAACCCACTCCTCTGCTCTAGCGCTGAGAACATAACACAGTATTGCCTTGTGAAGGGCTAAGCGGACGA  
 27693 TTCAAGAGTAAAGATAACTGTTGGTGGCTGCAGCACCTAGTACTGATGGTTGTAGGAAACACCACAGGCAGTATAACATGTA  
 27785 AAGCAAGTTCTTGGGTTCAAGTAAATAGATTCCACTTGACACGTGTTCACTCTTGGTGTGAAAAATTAGGAAAGGTGATAGGCAGGAT  
 27877 AGAATAAAATGAAGTGGTCCCATCTCCATATGGAGAGCGCCTGCCTCCACCACAGACACATGTTTGCCTGGAAGCATAAACAGAAGATT  
 27969 GCAGGAACGCCCTTCACCTCCATAGCCTCAGGCTCCATCGATAGCATCAAGATAAAACTGGTGGCAACAGACACTGAGCCATCATCTT  
 28061 GTTTAACATTTCACCTGGAAGTGGAAATGGAATCCAGAGAGGCTAAGTAGCTGCACAGCTACTTAATTGAACCTAGAACCAACCCAGTT  
 28153 TCTTAGTATTCTGGTGCCTTATTTATATAACATAGACAGCTGATCATGGTAGTTGGATCATTGCTAAAGACCTATTATATAACAAATCG  
 28245 TATGGCTAAGAAGATTAAGATGCTTATTTCGTTATCCATGATTAGAAATGTAATAAGAGACTTGTCTGTCACCAACAGAAGAGACAA  
 28337 GACGCCCTTCTGCTGTGGTGTGAGTGCCTCATCAAGTGCTGAGATGTGACTCATGCTTGGGAAAGTAGCAGATGAGAGAGTACATTC  
 28429 TATTCCGACTCCATAGACTTAACGTGGAGACTGAGAGTAGTGGAGAGCTCAGACTGACAAGAACAGAACATAGACTAGAGGCACCAG  
 28521 GCATGAAAATCATAAAGATGGAGATGACTTCTATCTGTGAAATGTCTGAAAAGCCTCTCTCTGTTCCAAATCCTCATCTCCAG  
 28613 CCCTCATCTGCCACCATCTGCGTTCTCCGTGCCCTCTCTGTCACCTCTCAATGTTGGGCCAGGATTTGTCTCAGA  
 28705 CTCACTTCAACCTCTCCCTCAGGACATCTCATCCACTCCAAAGGCTGGAACCTCAGCCTCCTCTCAGCCTGCGCTTAAGTTCATCCCT  
 28797 TTAGCTGTCTATTGGATGTTCCAGTTGGAAATTCCACAGGCATCTACCCAGGCTCTACACAAAGATGATAAAATATTATCATCTT  
 28889 TTTGGCAGATTGTTTCCTGAGTTCTGCGTGTTCATGGATTCAACCATTCAAGCAGGCTGCCAAGCTAGAAATGTGGATTGTTAAT  
 28981 CGGCCCTGCTGTGAGACTGGGAGGCTGGTGTGATAACCCAAGAAAGACATTGTGGCCTCTGGGCTTATCCTTTAACCCATTGCCTCAG  
 29073 CCCTGCCCGAGTGTGATGTTCTGAAATGTTGAACTCATTTATCTCTTACCTAAAGGTTGCAGGATATTAGATTCTGAATGAAATCCCC  
 29165 AATCCTTTTTTTTTTTAAGTGAAGCAAGTTATAAGAAAGTAAAGAAATAAGAATGGCTATGCCATTGGCAAAGCAGCCCTGTGG  
 29257 GCTGCTGGTGCCTTATGTTCTGATGATATGCTAAACAAGGGTGGAAATCCCCAATCCTGGCATTCAAATCCCAGACT  
 29349 CATTCTTTCACTTTTTTTAATCATGCCCTGCCTTCAGTTATGATGAGTGACTTGGTCATTGCTCAGGTGTGACTTGTCCCTTGC  
 29441 ACCTGCTGTGCCCTCTCCTAGAATGCGTTCTCCTGGCAAGTGTCTTCCAAATGGGCTTCCCTGGGAGGTGGTT  
 29533 CTGACGACCACCCCTAGTCCAAGTCAGCTCCACTGTACTTAAACTTCTCTTGTCTTCTTATTACCTGTGATATGCTCTCCCCAC  
 29625 CTGGTGTCCCTGGGACTAGGGACTTCCTCATTCACATTACATAACTTGAGGGCCTGGCTCATAAGAGGTGCTTAATGAATATTATG  
 29717 AATTAATTAGCATTTGCTTCAAGATCAGCCATCATTCTCTATCTCATCATTCAAATATATTCCCTCTTCCCTTGCACCC  
 29809 AGTCACAGACTGGACTCTATTAAATCCTGTCTATCATCTGGGCTCATTCCATCCTCAGTGTCTGTGCATCCTTCAATTGCCAGG  
 29901 GATGTTAGCTGATTCTGCCCTTCATTCCAAGCCTGTCCATATTCCATTACTTTATGAAGCCTTCTTGACACACAGATGCTTAATTAT  
 29993 TCTCTTTGCTTCTTGTGACTTGTGACTCTGCCACTGGTGTGAGCTTCAGAAGGGCAGGGATCTCACCTTCACCTCTTTCTCCT  
 30085 AGTGTCTTTGCTTGTGCTGCACACTCCCTGGCACACACAGCGGCTCTCCACACGAGGAGCTTCCAGCAGCCTCAACCTCAGGACT  
 30177 GGGCAGCTTTAAATGTATTGGCACCTTGCAAGAAAAGGATTGTGTTAAATGTAATTTCATGTATCTGTTATCAGAGTGCAAGAGAA  
 30269 GCAGAAATCAAATGAAAAGCAGAGTCAAACCTTTTATTGGACCCAGTGCCAGGTAAGAACTATCTAAATGTTAAATTAA  
 30361 AAACCAAATGTGGGAGAGAAAATCATGATGGCTTATTGTTATTGCTTATTGAAAGGAAAACAAGCAAATAACTATAGA  
 30453 AAATTGGGAAAAGAGGAAAATAAAATGTATAATCTTACCATAGCATTACTATTGTGAATATTGATATTCAATAGATGTTGAAA  
 30545 ATTGGGAGAGATTGAAAGACATTCTCAAGTTCAACAAAGAACATCTAATTACCTGTAAAATAACCATCAGAAAACAACAGGTATCAC  
 30637 TGCAGTTGCCTGGAGTCAGTGATAATTCCGACTAGCCCAGGCTCAGGCTCAAATACAAACCTTCAATTACTCTAACGATAAGTACT  
 30729 TTTCTGTTCTCACAAACCTCATACCACGTTGATGTGTTTATATGTCTATATTGTTATTGCTTTAAGAAGTTTGTATTCTATT  
 30821 GTAAAATACATAATATAAAATTACCATTTAACCATTTAAGTGTACGGTCAGTGGCATTAAATACATTCTCATGTTGACAAACCA  
 30913 TTACCAACATCCATTCCAGAACTCTTCACTTTCCCACACGGAAACTTGTATCAAATGATAACCTCCTCTTCCCATCCCT  
 31005 AGTAACCTCTGTTCTACTCTGTGAACCTGCCTATTAGAACCTCATAAATGTGGAATCATACAGTATTGCTCTTGTGCTCTT  
 31097 AAACCTAACATGTTCAAGGTCAATCCATGTTGCTAGCATGTGTCAGAATTCCCTCCTTCTGTGGCTGAATATTCCATTGTATGATATA  
 31189 CTACATTATATATCCTGAAATCTGTGATGGACACTGGTGGACTTGTGATGGACATTGGTTTGTGTTCATGATCATATAATTCA  
 31281 AGCTCTGTATTTCAGTTCACTCATTGAGTAGGTATACCATCATGTTTTTTTTTTTTTTTTGAGGCAGAG  
 31373 TCTGCTCTGCGCCAGGCTGGAGTCAGTGGTCAATCTGGCTACTGCAAGCTCCGCTCCTGGGTCACACCATTCTGCCTCAG  
 31465 CCTCAGCCTCCGAGTAGCTGGACCACAGGTGCCACTACCACACCTGGTAATTGTTGTTAGAGACGGGTCTCACTGGG  
 31557 TTAGCCAGGATGGTCTGATCTCTGACCTGGTGGAGCCAGCCTGGCTCCAAAGTGTGGAATTACAGGCGTGAGCCACCGTGGCCG  
 31649 GCCCATGTCTTGACCATGTTAAACTATGTGTTGTAACCTACTATAAACCATAGAAACCGATTATAATAGCAACACTATTGTGAGTAAA  
 31741 TAAGTGTATATAGCTTTCCATATTGTTCCCTGGATGCTGTTTAAATGAGTTTTTAAATAGAGCATAACTTATTATATGT  
 31833 TTACATTTCCTTAAAGAAGCTGACTTCTCATCAGCTGAGCCAGAAGTGAAGTCATTGAAAGAGAAGTTGAAAAAGGATCCTGTCAA  
 31925 GTGCAATGATTATCTTCAATTGCAATGCTGTTGCCAAAATGAAGAAGGACCCACTACAAATGTAATTTCATTAAAAAAAC  
 32017 ATTAAAAAAATAGGCAGAGGTTCAAGATGTACCTTACAGTGCAGCCTGGATAAGAAATCCTAGTCCCTGGTATCAAAGAGGTGAGTGC  
 32109 TTTGGATCAGGATATGGAGGTTGTTAGCCTGCAAGGACAGGATGTCGTGATGGAAGATGAGGTTGTCAGCTTCCAGGA

FIG. 12B  
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32201 GACAGAGTTCATCTTAGATGCTTCAGGGAACGCAACTGTGTTCTATGGAACATACATTACGTAGCAAAACACATAAAGGTAAAATAATTG  
32293 TTTTGTGTTCTAAATGTTTATAAGCTAATTCTCTGTATGCAGAAGGATGAGACTGTTAGTAGTAATTATGGCAACAGTCCTAA  
32385 TAGGTCTTGTCAATTCTCTTTGATAGCAACATTCTTGTCCCTGTTGAGCCATGGTATGCTATTGGATTGTTGTTCAGGTGA  
32477 ACCTTCTTGTACTCTATCCCTGTTGACATAAAATACAACCGGAAGATTCTGCCGATTCCACGTAGACCTGAACCATTCTCAGTGA  
32569 GGCACATGCTCGCCACCACGTCCCCGGCGCTGATGAATGGCAGTGGGAGGCCATCTGCCCTCAAGGGCATCCTCATGAAGCCGCCATG  
32661 CAGTATCCGAAGCAGGTGGGAGTATGAGCCAGCATTCCACTACTCAGACTCAGTACCTTGCTACCTAAATGCACCAAAATGCTCAA  
32753 TTAGACCTTGTAAATGCACAAGTGGGTCAATTAGACTCTTAATTAAATAGTATTATTAGACAGTAAAGCAAGCTGAGAAATAAGTGGCT  
32845 TTTAATTCTCTTCTTCTAAAGTCTCCTAGTTACCTCCCTACCAAATAGACTTTGAGCAGATGATGAACGTGTTGTCAGCTAA  
32937 CTAGTTGGCACTGGGTGCTTTACTAGTTGCTCTGTTCACTGTTCTTGCTGTTAATGTTATGGGATTGTTAACGTAGCTGTGAA  
33029 TTCTGCTTACTGAAGAAAATTGTTGCCTCTAGGAAATATTTCAGTCACTTGCCCTCATCCAGATATATTCTGTCAGGCCAGAATTGAAA  
33121 AAGTCCTTCAGGGGAGCATTGCGCTGAGCCATATGAAAAGTTCACTCTTAAGGTATGAATGGCTTTACGCTTGGG  
33213 GGTAAAAGCAATCTGAAAAGAGGCCATTATGTGATACTATAAAATCTTAATGAAATCAAACATAAGCCATATTATACTCTAAAAGATGTA  
33305 GAATATGCTACCTGTATTACTCTGAACCTTATGTCTGATTGAGGAAATGTAGTCCTATGTGTAATAAAATGATCCACTGACTAGA  
33397 CAGTTCTGACATCCTAAATAATTGCAAAGGAATTACAGCTTAATAGTAAACTTCTGTTAGAAGGTACATGTATGATATTCAAATAG  
33489 AGTTCTTCTATCTGTTAATTGCTCTTGGGTTCTGAAATTCTATTGTCACCTTACACTTATATATGAGGCTGGAGACCAGGAGATGC  
33581 CCTTGGCTCAGATGACCTGGCCAGCAGTGTCACTGATTCACTGGTTCTGCTAGAAGGGCAGAGTTTAGGTGGAAGATGGAAA  
33673 GAAAACATACATGATGTTGTTTCAAAAGTACTGAGGAAATGAGGCTTAATAGTAAACTTCTGTTAGAAGGTACATGTATGATATTCAAATAG  
33765 TATTAGAGGTCACTAGTCCAAGATGTGCTTCAATTTCAGGACACTGAGGCTCACCAAGGCTTAGTGATCTGCTCAGTGTCTCATGGCTG  
33857 GAGCTGCCAGGGGGCACTGACTGCCACTCGTAGCACCTGTGCTACCTGGTTAGTGTAATCTGTTAAGTGTCTTATCCTGCCAGTTT  
33949 ACATATTAGTTATTAAAAAAATTGTTGCTGTCATCTGAGAGGCCTGAATTCACTGACAAGGACTGGCAGCAGTAGGAGTGGATAC  
34041 CCCAGAGGCTGTGAGTGAAGTTACTAAGTGGATTCAAGAGCTTCTATTCACCTCTATGGCGCCATGCATCACAGCTGTGCCACAG  
34133 GATGCACGATGGCATTGAGAAATGGATTGGAGTCAGAAGACCTGGGTGCTGATGCTTAACACTCATCTGGGCTTGGACAAATCACAT  
34225 CACCTCTCATGGCCTCCATATGTCCTCTGTCATGAAGGATGATGTTACTTCTGCCTCTGCCCTCATAGGGACAGTGTAGGATCA  
34317 AACAGATCATGTATGAGTCAGTGTGGCACCATAATCACAGAAAGCCCAGAAGACATGTCATTACAGCCCCAGTCAAGTAAA  
34409 GCCCAATTACCCAGGCACATTGGTCCAACAGTAAGCCTTTGGCTGATGAAAGCTGTGAAAGTTGGCTCTGGAGAGAAGCTGTTTA  
34501 TTTTTTAAACCAAGTCTGAAAACCTTGGATGAGAAGCTCTTCTAGCTTTATGTTGATCAATAATCAATGAAGGCCAATATAAGA  
34593 TCTCCTCCCCGACCGTGTATGCAACACATTCCAAGGCCATCCACAGCAACTTGTACTTCTGCCTGCCATGCATGGTTGAAATT  
34685 GGCAGCTCATATTGGTAAAATCACATACACTGTAGGCTAAACTTACCTCTGCACACTCCTCCATGTCACACTGAGCATCTGCTGAAGTC  
34777 TGCTTTCTCATTTTATGGAATGTAAGCTCATCCATGTGTCATTACATGCATTACTTTCTGCCACCTCAAAGCATTCAAT  
34869 TAAAGCAGGAATTAGGCTCAACTATCTACTTTAGCACAGTTGGCAGAGATGTTACAGTGAGATGATTGTTCTGTCTGCAAAGTTG  
34961 TTTCTCATGTTCCAAGATGGCTAGAACATCATTAGAGTAAATTTCATTGGAGGAAATTGAAAGCTCTGTAGGTATCT  
35053 CCTGTGAATAGAGGTTAAAAGAAAAGAAGGGAAAAAGCCAAAGGGAAAAATAAGTTCTACTCTGACTTCACACATACTGTG  
35145 TTCTATTGCTCCCTCATATGTCGAGAGCTAAGTCCTCATTCACTGCAGAAAGGCTTATTGATGTTATGTTAGCTTAAATT  
35237 TGAAATTACTGCATTACTCCACAACATATTCACTATTGTTAGAACCAAAATCTGAAACCTGAAATGTTAAGTAAATTGACCCCTGCA  
35329 GCTAGGTAGGCCATTGTACCCCTATAACTCATACACCTAACAGACCCCCTAACAGTCCCCCACCAGGGAGGCAAGAACATACCTCATTGGAGAA  
35421 GGGGGGAGGTCTAGATGATTCCCTGACATCTCTTCAATTAGGATGTTAGGTACTCATGAAGGCAGCAGTCCTACAGCATGAT  
35513 TATGGTAGGATTATAAGTTGCAACTGAAAGGGATCATGAAAAGTATAGCCTAGCCCCATTTCAGGTGTTAGTGGAGCTCAGAGA  
35605 GGTTTGATGGCCTACAGAGTCATACAGCTGGATTCACTGTGACTTAGAGACAGACAGCTCTGTCATCTAGATCCTCTGGATCCTCTAGAT  
35697 CCTTCCGTGGCTGATGGTACACACAGATCACCAGGCTTGTGAGAACGACGCTGATCCAGGAAGTTGGGCAAGGCCTGAGACTC  
35789 TGCATTCTACAGTGTGCTATAGCACACTTTGGTTGGAGTACATTCCAAAATTGGTTGACTTGATATACTTATGTAAA  
35881 GACCCTCAGTAAAAAAAAAAATTAGTAATGTAAGGACCTTCACGTAACTCTGAGACAATCAAACATTGCTTGTGACA  
35973 AAGCACTATCACAGTACAGACAAATTGAAAATTAGCATTATCTTTTAGCAATAGGGTATAGATGATTAATAATAGGTCTGCCCTA  
36065 GGCTAAAAGCAAATAAGCTCATTTGACTGAAATTCAATCAACAAACAAACAAATTGATCATTAGGAAGTAGAAATAGCAG  
36157 TAATTCACTGTTAGAAAGCAAGAATATAGCATTGAGAACCCAGCCTAACGTGAGTCAGTATCTTAATATCTTATCCCTTATATTGTGGGAA  
36249 TCAGCATAAGCTAGTGCCTTACGGAGCTGTGAAAGCTTAGTATTAAATTAGTGTCTCATTCATTCACTAAATGTGATATATTGAT  
36341 ATGGATACCAAAATAGTAATTATAACTCAGTAGACTTATAATAAGTAGCAGCTAGTCATAAAAGATGTATGAAAACCTCTGAAACAGCAT  
36433 GTTGTGCCCCGAAAGACCAAAAGAAGAGACATGGATTGGAAAGTCTCGTTGTATTCTTGTGAGAACACTGCTAGAGAATGCGTAA  
36525 ATAAAGTACTCTGCACAGAGTGTGAATCCAGCCATATTCACTGTGATGTTGCTTTCTATGCATCCAATGCTATGTTAGGACTTATT  
36617 TAGTGAGCATGTAAGGATGGCTTGTGAGGTACAGTCTTCACTGAGATGCACTGATCTCATAGCTTATTCTCATGTCTCAAGGTGGCCC  
36709 AGAAGGTGCTGAAGAATGCCAAGCAGGCATGCCAAAGACTAGGACACTATAGAATGCCATTGCTGGCAGCAAGGTAGGAACACCTTT

36801 ATACCTTTAAATCGATATAGATAGGTGCATGGATGGTCAATAGGCCTATTCTGTTGTCAGAGACAAAGAGGATTGAATGTGAA  
36893 AACTGAGAAATACATAAGCCAGATTTGAAAAATCATTGGTAGAGTCACAGAGAGGATAGACACTGTCGGAGAAGTGCACCTGGAAC  
36985 TGGCAGGGTGCACGGTAGTGTAGCTGCAGAGCTGGATTCAAGGACCCACCACATGCCTCCAGCTGGAGTCAGGGCAATCCAGTGAGC  
37077 CTGGGTGATCTTATCTCTGACTCTACTTGTAAAGCATTGACTTGTGTATATTGTTCTAAGCACAAGCCATTGGCTGGAACTGTTT  
37169 CTATGTAAATTGATTAGTTGTCCTCATCCCCATAGATGTTCCATGTTAGATAATGAGATTCTGTTGGCTAGCCAATGGAATAA  
37261 TAATTAGACTCTCATAGAAACTAGACTTAAATAATGAATTGATTGGTTGGAAACCCAGTTAGAAATGTTGCTTGCCATTTCAG  
37353 GACATTGTTAAGGATGCATCTGAAATCTGACAAAAATGCCAGATTCTGCCATCTACAGGCAAGACAGCAATAAGCTATCCAATGATG  
37445 ACATGCTCAAGTTACTTGCAGACTTCGGAAGTGAAGTTCAAGGTCTTATTCCACACCTGAAAAATAGAAGCTGTAGTGGGGAGGGAGG  
37537 AACAGGGGAGCAGTCACTTAGGTTGCTCGATTAGACATCAGAGGGATGGCAAATGAGCGTGAAGCATTCTCAAACCCCTGAGAAGAAA  
37629 GATGGGTGAAAATCAGAAGAATAACCAGTTAATTGAATTCTGAGGATGTTGGGTGGCTGTGAAGGGTGGACTGGTAAGGATG  
37721 AGCCTATGGTGGGGAGGAAACAGTTGAGGAACCTTGTCAAGAGGTGAGAAAGGACTCAGCAAAGCCACTGCAAGTGCACACAGGAAGAAGGG  
37813 GACAAATTCAAGTCGTGCCAAGAGATAACGATGACTGGCTTGGCTGGTAATAGTCTAAGATAAAACTGCAAGGTTCTAAC  
37905 TTGGAAGTTCTGGCACCAGTTGTTGCTTAGTTGTGGCAGCATTGCTCCACTCTGCCTCTGGCCTCACATGGTCCCTTCCTGTGTCTC  
37997 TGTCTAAATTCCCTTCTAGAACACTAGTGATAAAGCATCAGGGCAAGCCTAGTGACCTCATCTTAACTGATTGCATCTGAGAGACCCCTG  
38089 TTTCCAATAGGTACATTAGGTACAAAGGGTGGACTTCACCATGCTTGGAGGACACAATTCAACCCATAACAATGAGGCAAAGA  
38181 GGGAGCAAGGAATGTTGCAACATCACAGGGCGGCAGCTCCCCAAGTCAGTCTCACCCGAGGGTGTGTTCTAACCTCTATGCTGTTT  
38273 TGCTGCTACATCTAAAGAGTTCACTCTGAACCTTGAAACTGATTCTTGTAGGGAGATGGCTTCTAGAATTCTGGGAAATTCT  
38365 GGGATGTGAAAGAGCTGAGGGCGCTAGAAGATGTGAAGTGAAAAGAATAGCTGAGAGGCAAATGCTAACTATTCTATGCCAAGGTATCCT  
38457 TGTTTTTTTTGTGCATATCAAAATAGCAATCTTACAGTTGCTTAGAACTCAAGAATGATTGCTTAGCTTCTTAAACCTTATT  
38549 TTACCTTTCTTATCTGTCAGTAGTAGGAATAGAAACGATATGAGTCATAGAAACAGGCTCAATAAGTCTGAAAACACAGAGACGTG  
38641 TTCCATAATCAGAATCCAATCACGTCCATGTCAGCAGGGCGCTTCAGCCTTCAGCGACGTGAAACCCCTGTCAAGAGGCTAAAAAGGTA  
38733 GAAAGGATTCTCAAGGTCTTTCAGTTATGTGATTATACAGTTTGACTGTTGATGTTCCCTGTTGGAGCTTAAATGAGAAGTGC  
38825 AACCTCAGTTGCTAACATGCAGCTAAGGTTGGCTGTCAGCAAAGCAGTGTGCATGCCGCTGGCTGATTGGAAATGAAACCTTCACA  
38917 GCTCACGTAGGAAATTGGAGAAGGGGAGAGGAGATACTGGTAAGGATGAGGCTGCTGGTTAGCCTCCAGGGTCTGGACCATA  
39009 GGTGCCCAAATTCCAGTCACTATCTGACAGTTATGACCTGGTAAGGACACAGGTCTGGCCAGGGAGTGCCCTGGATCCCTATGAAT  
39101 CTGTTATTGAAAGACTAAATAAAAGAATAGTACCCATTTCATTTAAATCATAGAGGTTCTTAGTTACAAACATAATACATGTT  
39193 CATTAGAAATTGAGAAATACAGAAGAATAAAAGGATGAAAAAGGTTACTACTAGTTAACCTCGTGGTAACCTTGAGAAGTGC  
39285 TTTTTTTTTGAGATGGAGTCTCACTCTGTCCTCAGGCTGGCGTACAGTAGCACGATTCAGCTCACTGCAACCTCCGCTCCGAG  
39377 TTCAAGCGATTCTCCTGCCTAGCCTCCCAAGTAGCTGGACTATAGCGCCACCACAGCCTGGCTAATTGGTATTAGAGA  
39469 TGGGTTTCAACATATTGCCAGGCTGATCTCAAACACTGCTGACCTTGATCTGCCCGCTCAGCCTCCAAAGTGTGGATTACAGGCAT  
39561 GAGCCACCGTGCCAGCTAGGGGGAACATTTCAGTTTATTCTTACATTGTTATTTAGTTATCTATGTAGCTATGATCAT  
39653 ACTAAATATGTAATATTCCCTGCACAACCTCAAGTATTGAAAGTGTATATACATTTATAGACATCTTAAATGCATAAATA  
39745 TTATAATAGTCATTGAGATAGACCATAGATTATTAACTCTCCCCATTGGACTTTTTCCGAGATGGAGTCTCGCTCT  
39837 GTCGCCAGGCTGGAGTGCAGTGGCACCATCTCAGCTCACTGCAACCTCCGCCCTCCAGGTCAAGCAATTCTCCTGCCTCAGCCTCTGAGT  
39929 AGCTGGACTCCTGAGTAGCTGAGTAGGCCATGCCACGCCCCGCTAATTGGTTTTTTGTATTAGAGA  
40021 TACTAAATATCTCACCCTTGCAGGCTGGCTCAAACCTCTGACCTCAGGCAATCTGCCCGCTCAGCTCCAAAGTGTGGATTAC  
40113 AGGTGTGAGCCACCATGCCAGCCATTGGTACTTTAATGTGTTCTGATTTCAGAATTACCTATAAGCCACAGTTAGAATCTTAA  
40205 AAAAATCTCTTATGGTAGGGTAATATATTACATACACTATATTACATATAGTAATTGTCATTGGTAGTTCAAGAAA  
40297 ATTCATTCTACTAATTTCAAAACAGTCACCTTAGTTGGATAGATTCAATATTCTCGCTCAACTACCATGCAACTCTTAA  
40389 TAACCATGAGGTGGCTGCGTGTACTTAGGAAAGTGAATAACACTATATTAAAGGAAGAAAAATATACTGTATTACTATATTGAA  
40481 AAGAAAATATATATTCTTTGTATGTAAATGAAGAAATGGATAAGCAAGTAGCTATCTAGATGGAAAGATAGGCATAAAAATAGCTATT  
40573 GGATATATGCCAATAATCATGGTTATCTTGAGGGATGGGTGATGGTGTATTACCTTACATTAAACATTGTCTTATA  
40665 TGAACCTTTAAAAACTAACACTTTTATATTCAAGACAAAACAATGAAGTTTTATATGTGATGGAGGTTGGAGCCCTGTCTCAGAAG  
40757 TTACTCCTAGGCTGGTAGCTGAGACTTCCCACAGTGGGGCTCTCAGGGCAGGCCAGTGCATGGCCTGTCTCAGTGGAGGCTG  
40849 GGGAGTGGGCTTACATGGTACTATTGAAAGTGAAGGAGCAGAAAGCCTGAGGCCAGGAGGCCAGGGAAAACCAAGTGT  
40941 GAGTTCTCTCTGCACACCCTCTCATGTCAGTGTCTCAGCAGGAGGGCATTGGTGTGAAGGGTGTGCTCCAGGTGGCCAGTTAGAGACCC  
41033 AGAAACCTGAAAACAGGGATCCGATGGTACAGCATAGAAGACACAGCAGGATAAGTGAGGCCACGCTCCTCAATAAGTATTCAAAGAAA  
41125 TTGGTGCCACTCCCCGTATTCTCACAACAGAGTTAGGGACGTGGAGGATTCTTCAATTGTTAAAAATCTTGCAATTGCTATT  
41217 CTTCCCTCTGTATATTACAGGAAATACTCATGTCAGTGGCCTGGCACCGGCTGGATCCAAGCTATTGTTCTACCCCCATGATTG  
41309 TCTCAAAATGTTATTAAATGCATGAAAAATTCTTACGCTGTCTCAGCTTAAACAAACAGCTGCCAAGCTCATAAGCCACTTTC

41401 CTTTTCCCTGCAATAATTACCCAGGGATATGTTCCAAGATTTAGTAAGAAAGCGATTCTGTCCGATAGATGATATTGCTAACATTATA  
41493 AGAAGAGAGACTTGGTACTTTGTATTGATTGTTCATGGTGGTATCTCATGGATAAGATGGTATCTCATCTTCCAACCTCTGCAGGAAA  
41585 TGCAGAGACATGAAGGCAAAGTATAAAATAGAACGTTTCTTAAAACGTAGACCTTTAATGGTACTACGTTGGATAGTTAGGTAAATA  
41677 ATACTACTAAAGTTTGCATGCAGCTTAATGTGTCTGTGTTATTGTACACTCATCTTGCATCCAGGTTACAGTCTTACCC  
41769 GATTCGCTCTGGTTACACTGCACCAAGCTAGGGCTGCTGACTTCTCAAACCCACTGGGACTTCCCTGCCATGCTTTCTC  
41861 TCTGCCAAATTGTGTCCTTCCTGCCTCATCAAGCAGCACATAAATCAAACACATGCAGCATAACACACTTCCCTTGCCT  
41953 TCTCAGGGAACTCTACTCATCTTCAAAGCCCAGTCTGTCAGCTACTTCTGTGCTGGAGTCCTGGAGGCGTTACTGGCTCTGCCTG  
42045 AGCCGCCCTCCTCTTTIAAGGGTGGATAATAACAGCCCCTGCCCTAAAACCGTGGTGGGAATAATGCAAAAGGCATTAAGGTGATT  
42137 TCCCACCATGAATACTGATCTCATCCGTGTTCCCTCGATAGATCTAGATACTGCCTCTGGTAGAGGTTGTACATACTGTGAAA  
42229 GTGATTGCCCTCATATGCCGTAAGTAGCTTACAGTGTACTGGACTTTGGCTCTGGAGGAAAGAAATTATGTTGCAATTCC  
42321 ATGGTCCTGAGTACATACATTGCAGCATATCCTAACGACTTGATAAAATGCTTATTGAATTTCCTTAGACATAAAACTCAGTGGTTTGT  
42413 TGAAACAAAAATATCTCAAATTCTTCAATCATATATAGTTGTTTTAAAGTGCACACAAAGCTTTAGGGATAATTCCCTTCACAA  
42505 AACACAGTTAGAAGATTAAACTCACCACCAATAGCAGTCCAAACATACCTGTATTGCCAGCTAATTTAACGAGCCAATACAGGAAGTC  
42597 AGGAAGGGAAAGACCGGCTGCAGAAACACTTAGATAAGGACCCAAATCTGGCATGGGAGGACTGCTAGTTGATGATACCATTCCATT  
42689 CCTCTGTGGATTGTTGAGTCAGCAGAAATGGATGGCAGTGGGAAGGGAAATTTCCTAACAGAGAGGTTGAGCCTCACTTACATT  
42781 ACACAGAGACAGGAGCAGTCCCAGAGGCCAGGCATCCTGCAAGTGTCTGTATTGCATGCTTACTTAATCGTGAATTAAAGATGAGTT  
42873 TCATGTTCAAGGATTATTTATAAATTTCATAGAATATAGGTACTCTTAGCAAAACAAAGCAAAAACCAAAACTATTCTCAGTCATG  
42965 AAAGAATTCAAGTTGTGTAACACGCACACAACCACCTTGGAGTGCATAAAAAGGCAGTAAAATCTTATTGCCTGTGAGTGGATG  
43057 TCTAATAAACCAGATTCAACATAAACATAACTTTGAAATGGTTGAGATTGGTTTAAAAACTAAAGCTGGCAAAAAAAACA  
43149 ACTTTAAAGCCATGTCTACATAATATGGAACACTAAACTCAGAAATGTGCTGGAAACACATGGAAAGAACGTCTTACAGAACGCAA  
43241 CTAGAAGTAAATCTCTCAGCAGAGGGAGGAAATAGAATAAGAAATAACTATAGTTAGGCACAGAAGGACACAATACACTATAGGAAGATT  
43333 CCAGTGAAGATCATTAAATTAAATATGTTGCTTAGAACGTATTTAATTGTGTTCCACCTCTCAAAATTTATATGTGGAGGATGTTG  
43425 GAGTGATCTAAAAATGGTGTGAGATGCCTGTCATTCATAGGTGGAAATAATTAGGAGGGGTGAAATCCATTACCTGCATACTTAC  
43517 TTATATTAAAGTATAATTGTAATAAA

hCLASP4	-----MFPMEDISISVIGRQRRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG	41
hCLASP2	-----MLLFPLYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
	...	
hCLASP4	-----STVPEDAEKRAQSLFVKECIKYSTDWHVVNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVLEDYLITHPLAVDGPLRDLIEFP	83
hCLASP2	-----TVPAKAEEEAQSLFVTECIKYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAAATVSWDIRTLYSTVPEDAEHKAENLLVKEACKFYSSQWHVVNYK	120
	::	
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDDLVVFTPKECTRLQPSLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRQLPNKVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLQPRECRTTEP-GIPKD-EKLDDAQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG	180
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hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTLQPDGSYILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGPEDSNDSRRGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSCT	239
	:: . . :* : . : . : . .	
hCLASP4	DVQCPKMRRAFELKMLDKYSHYLAATEQEMEEWLITLKKIIQINTDSLVQEKKETVE	222
hCLASP5	DVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARPN-----RQAE	169
hCLASP3	DDTPRGSWACSIFDLKNSLPDALLPNLLDRTPNEEIDRQNDQQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAAMQEK	219
hCLASP7	EDTPRSSGASSIFDLRNLAADSLLPSLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNDLTYFVLAATESDMDEWIHTLNRLQISPEGPLQGRRSTEL	299
	* :* : . . : . : . .	
hCLASP4	TAQDDETSS----QGKAENIMASLERSMHPELMKYGRETEQLNKLSRGDGRQNLFSFDSE	278
hCLASP5	LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD----EEEPIERLSVPDIKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD----EQSKLEGSGSGLDSYLPPELAKSAREAEIK---LKSESRVKLFYLDPD	272
hCLASP7	LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE	273
hCLASP1	TDLGLDSDLNSVTCECTPEETDSSENNLHADFAKYLTETEDTVKTRNMERLNLFSLDPD	359
	· . . . : . : . : . .	
hCLASP4	VQRDFS----GIEPDIKP-FEEKCNKRFVNCHDLTFNILGQIGDNAKGPPTNVEPFFI	333
hCLASP5	IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARSAVFV	268
hCLASP3	IEPIFAS----LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDLSFNLQCCVAENEEGPTTNVEPFFV	327
hCLASP7	IEPIFGI----LALYDVREKKKISENFYFDLNSDSMKGLLRAHGTTPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKKDLLEPESVIKPFEEKAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV	419
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FIG. 13  
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FIG. 13  
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FIG. 13  
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### Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYLSDEYCKHHFLVGILLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSCSSFQDQKIASMFDLTSEYRQQHFLTGI	1085
hCLASP3	LFTEI	
hCLASP2	PCSLLTTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFRQQHYL	1196
hCLASP7	AGIVLTELAV	
hCLASP1	PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGILLREVGT	1052
	PCCPLSPPASPSPSVSSTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAG	1119
	ILLTEIAL	
	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIG	1157
	ILLREVGF	

hCLASP4	ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQLYLPFVGLLENIQRL	1116
hCLASP5	ALDAEGERGISKVORKAVSAIHSSLSSHDLDPRCVKPEVKVIAALYLPLVGIILDALP--	1143
hCLASP3	ILDPAEGLFGLHKVINVHNLLSSHDSDPRYSDPQIKARVAMLYLPLIGIIMETVP--	1254
hCLASP2	ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRI	1108
hCLASP7	ALEPEAEGAFILHKKAIISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP--	1177
hCLASP1	ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAAQIASLYMPLYGMLLDNMPRI	1213

hCLASP4	AGRDTLYSCA-----AMPN-S-----ASRDEFPCGFTSPANRGSLSTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----	1162
hCLASP3	-----QLY-----DFTETHNQRGRPICIATDD--	1276
hCLASP2	NVRDVSPFPVNAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAIISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSRLASMLDSDTE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTFSKDVLNIAAFSSIAIS	1273

hCLASP4	FQ-NGHGIKREDSRGSLIPEGATGFPDQGNTGEN-----TRQSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVAlAIAGNNFNLKT-----SGIVLSSL PYKQYNMLNADT	1208
hCLASP3	-----YESESGSMISQTVAMAIAGTSVPQLTR----PGSFLLTSTSGRQHTTFSAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGN SVVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALS AES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDR LDQAE	1327

hCLASP4	RSLLMCYLYIVKMISEDLLTYWNKVSPQELINILILLEVCLFHFRYMGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETQLQKWFDTLSVLQLNRLLDLYLCVSCFEYKGKKVFERMNSL	1384
hCLASP2	IKSLLMCFLYILKSMSSDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEG	1287
hCLASP7	SRTLLACVLWVLKNTEPALLQRWATDLTPQLGRLLDLYLCLAAFYKGKKAFERINSL	1309
hCLASP1	TRSLLMCFLHIMKTISYETLIAYWQRAPSPEVSDFFSILDVCLQNFRYLGKRNIIRKIAA	1387

hCLASP4	WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEGARGEMMRRRAPGNDRFPGLNEN---	1311
hCLASP3	TFKKSKDMRAK-----LEEAIALGSIGARQEMVRRSRGQLERSPSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSLDMKAR-----LEEAIALGTIGARQEMVRRSRERSPFGNPEN-----	1350
hCLASP1	AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTS RHEGHKQHRSQTLPIIRGKN-----	1442

hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTAELDQEALISGNLATEAHЛИLDMQENIIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEANЛИLDTLEIVVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTSDRVDKTDMEHEALVEGNLATEASLVVLDTLEIIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDLVSLFTQTHQRQLQ	1500

FIG. 13

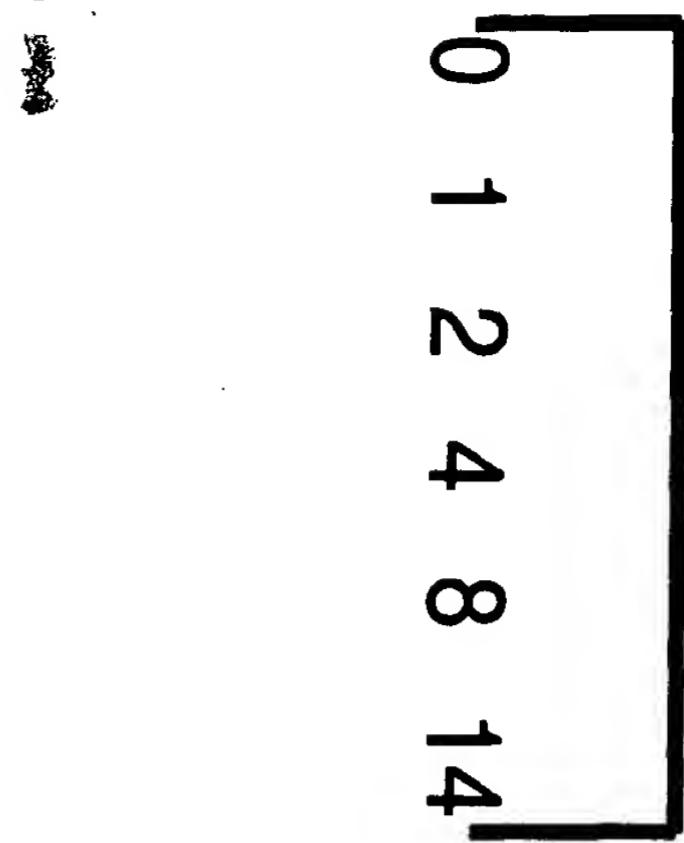
FIG. 13  
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<p>hCLASP4</p> <p>hCLASP5</p> <p>hCLASP3</p> <p>hCLASP2</p> <p>hCLASP7</p> <p>hCLASP1</p>	<p><b>ITAM</b></p> <p>EKFGTENVKIIQDSDKVNAKELDPHYAHIQVITYVKEYFDDKELTERKTEFERNHNISR 1799</p> <p>QCFGAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEBYFDEYEMKDRVTFEKNFNLRR 1810</p> <p>ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEBYFDTYEMKDRITYFDKNYNLRR 1932</p> <p>DKFGSENVKMIQDSGKVNPKDLDHYAYIQVTHVIBFFDEKELQERKTEFERSHNIRR 1770</p> <p>ERFGDDVVEIIKDSYPVDKSKLDSOKAYIQITYVEBYFDTYELKDRVTFDKNYGLRTFL 1851</p> <p>DKFGADNVKIIQDSNKVNPKDLDHYAYIQVITYVBFEEKEIEDRKTDDEMHNINRFV 1972</p> <p>: * : * : * : * : * : * : * : * : * : * : * : .. * :</p>	<p><b>ITAM</b></p>
<p>hCLASP4</p> <p>hCLASP5</p> <p>hCLASP3</p> <p>hCLASP2</p> <p>hCLASP7</p> <p>hCLASP1</p>	<p>FEAPYTLGKKQGCIEEQCKRRTILTSNSFPYVKRIPINCEQQINLKPIDGATDEIKD 1859</p> <p>YTPFTLEGRPRGELHEQYRRNTVLTTMHAFFPYIKTRISVIQKEEFLTPIEVAIEDMKK 1870</p> <p>YCTPFTLDGRAHTELHEQFKRKTILTTSHAFPYIKTRIVNVTHKEEILTPIEVAIEDMQK 1992</p> <p>FEMPFTQTGKRQGGVEEQCKRRTILTAIHCPYVKRIPVPMYQHHTDLNPIEVAIDEMSK 1830</p> <p>FCTPFTPDGRAHTELHEQFKRKTLLSTDHAFFPYIKTRIRVCHREETVLTPVEVAIEDMQK 1911</p> <p>FETPFTLGSKKHGGVAEQCKRRTILTTSHLPYVKRIQVISQSSTELNPIEVAIDEMSR 2032</p> <p>: * : * : * : * : * : * : * : * : * : * : * : .. * : * : * :</p>	<p><b>DOCK motif</b></p>
<p>hCLASP4</p> <p>hCLASP5</p> <p>hCLASP3</p> <p>hCLASP2</p> <p>hCLASP7</p> <p>hCLASP1</p>	<p>KTAELQKLCSSDVDMIQLQLKLQGWVSVQVNAGPLAYARAFLND SQASKYPPKKVSELK 1919</p> <p>KTLQLAVAINQEPPDAKMLQMVQLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL 1930</p> <p>KTQELAFATHQDPADPKMLQMVQLQGSVGTNVQGPLEVAQVFLSEIPSDPKLFRHHNKL 2052</p> <p>KVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNKRYPDNKVKLLK 1890</p> <p>KTRELAFATEQDPPDAKMLQMVQLQGSVGPTVNQGPLEVAQVFLAEIPEDPKLFRHHNKL 1971</p> <p>KVSELNQLCTMEEVDMISLQLKLQGSVSVKVNAGPMAYARAFLEETNAKKYPDQVKLLK 2092</p> <p>* : * : * : * : * : * : * : * : * : * : * : .. * : * : * :</p>	<p><b>Coiled-coil</b></p>
<p>hCLASP4</p> <p>hCLASP5</p> <p>hCLASP3</p> <p>hCLASP2</p> <p>hCLASP7</p> <p>hCLASP1</p>	<p>DMFRKFIAQCSIALELNERLIKEDQVEYHEGLKSFRDMVKELSDIHEQILQEDTMHSP 1979</p> <p>LCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNNKLKENLRPMIERKIPELYKPIFR 1990</p> <p>LCFKDFTKRCEDALRKNKSLIGPVQKEYQRELGKLSSP----- 2090</p> <p>EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKT- 1949</p> <p>LCFKDFCKKCEDALRKNKALIGPDQKEYHRELERNYCRRLREALQPLLTQRLPQLMAPTP- 2030</p> <p>EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMSELSTVMNEQITGRDDLSKR 2152</p> <p>* : * : * : * : * : * : * : * : * : * : * : .. * : * : * :</p>	<p><b>Coiled-coil</b></p>
<p>hCLASP4</p> <p>hCLASP5</p> <p>hCLASP3</p> <p>hCLASP2</p> <p>hCLASP7</p> <p>hCLASP1</p>	<p>WMSNTLHVCAISGTSSDRGYGS<del>PRY</del>AEV-- 2008</p> <p>VESQKRDSFHRSSFRKCE<del>T</del>QLSQGS----- 2015</p> <p>-----</p> <p>VLPNSLHIFNAISGTPTSTMVHGMTSS<del>SSVV</del> 1980</p> <p>--PGLRNSLNRAFRKADL----- 2047</p> <p>GVDQTCTRVISKATPALPTVSISS<del>SAEV</del>-- 2180</p>	<p><b>PDZ ligand</b></p>

# Human CLASP-2 expression in T cells upon activation

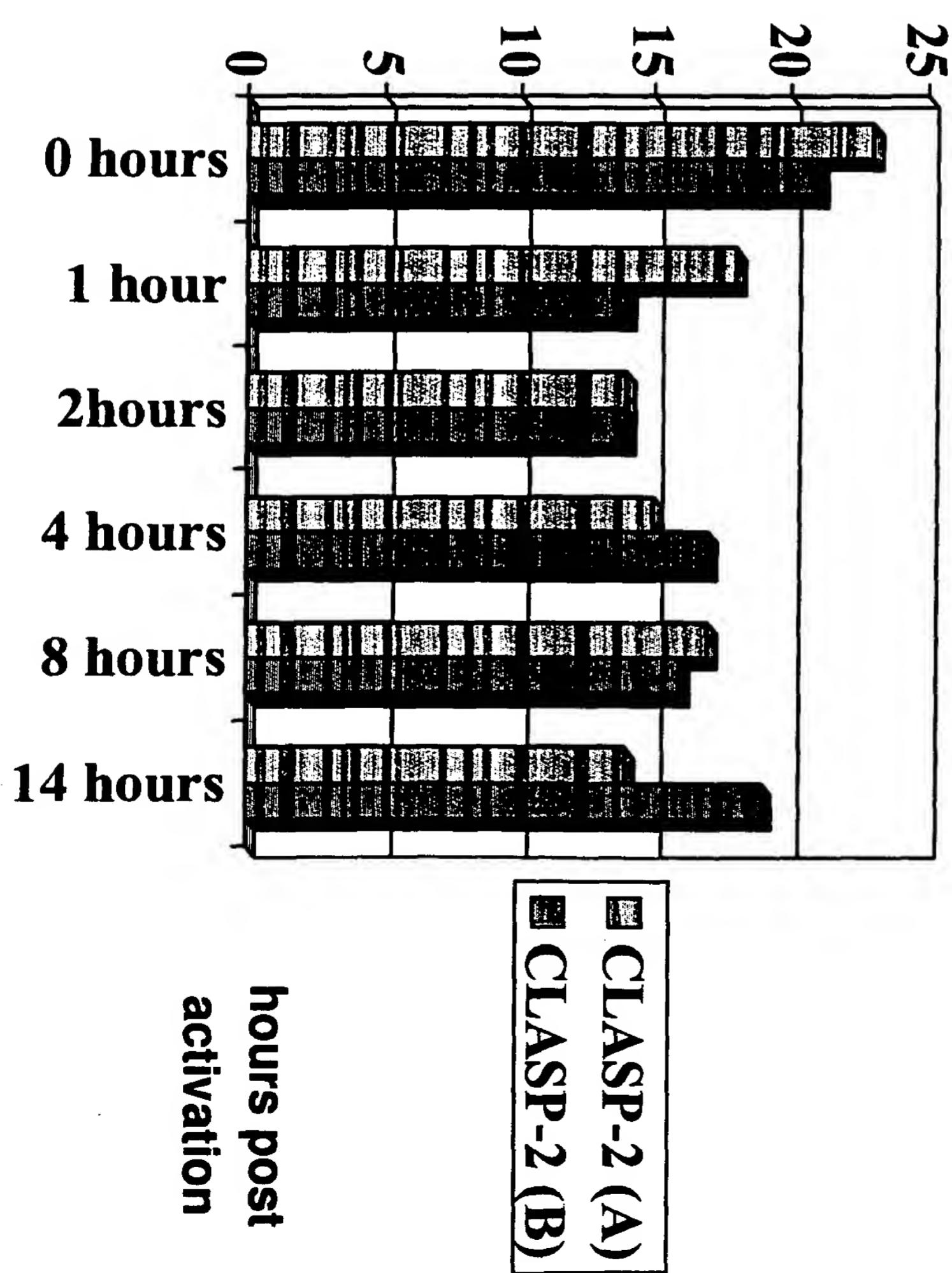
A)

hours post  
activation



B)

% of total  
signal



0 5 10 15 20 25

28S rRNA Ethbr. staining

FIG. 14